[redacted] 88611

STIC-Biotech/ChemLib

From: Parkin, Jeffrey
Sent: Monday, March 10, 2003 1:26 PM
To: STIC-Biotech/ChemLib
Subject: U.S. Serial No. 09/191,772

CF

Please search **SEQ ID NO.: 2** from the aforementioned application (**09/191,772**) v. all relevant databases, including interference. Place results on both paper and disk. Thanks!

JSP
AU 1648
CM01-8E15
308-2227

[redacted]

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:_____	NA Sequences:_____	STN:_____
Phone:_____	AA Sequences:_____	DIALOG:_____
Location:_____	Structures:_____	Questel/Orbit:_____
Date Picked Up:_____	Bibliographic:_____	DRLink:_____
Date Completed:3/12/03	Litigation:_____	Lexis/Nexis:_____
Searcher Prep/Review:_____	Full text:_____	Sequence Sys.:_____
Clerical:_____	Patent Family:_____	WWW/Internet:_____
Online time:_____	Other:_____	Other (specify):_____

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: March 10, 2003, 17:44:28 ; Search time 30 Seconds
(without alignments)
103.024 Million cell updates/sec

Title: US-09-191-772A-2
Perfect score: 77
Sequence: 1 RIQRGPGRAFVTIGK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	35	15	Q76740	Q76740 human immun
2	77	100.0	35	15	Q76741	Q76741 human immun
3	77	100.0	35	15	Q79439	Q79439 human immun
4	77	100.0	36	15	Q80545	Q80545 human immun
5	77	100.0	36	15	Q80546	Q80546 human immun
6	77	100.0	36	15	Q80547	Q80547 human immun
7	77	100.0	36	15	Q80548	Q80548 human immun
8	77	100.0	36	15	Q80549	Q80549 human immun
9	77	100.0	36	15	Q80550	Q80550 human immun
10	77	100.0	36	15	Q80551	Q80551 human immun
11	77	100.0	36	15	Q79428	Q79428 human immun
12	77	100.0	36	15	Q79429	Q79429 human immun
13	77	100.0	36	15	Q79430	Q79430 human immun
14	77	100.0	36	15	Q79433	Q79433 human immun
15	77	100.0	36	15	Q79415	Q79415 human immun
16	77	100.0	36	15	Q79416	Q79416 human immun
17	77	100.0	36	15	Q79417	Q79417 human immun
18	77	100.0	36	15	Q79418	Q79418 human immun
19	77	100.0	36	15	Q79419	Q79419 human immun
20	77	100.0	36	15	Q79434	Q79434 human immun
21	77	100.0	36	15	Q79435	Q79435 human immun
22	77	100.0	36	15	Q79437	Q79437 human immun
23	77	100.0	36	15	Q79438	Q79438 human immun
24	77	100.0	36	15	Q79536	Q79536 human immun
25	77	100.0	36	15	Q79537	Q79537 human immun
26	77	100.0	36	15	Q79539	Q79539 human immun
27	77	100.0	36	15	Q79540	Q79540 human immun
28	77	100.0	36	15	Q79542	Q79542 human immun
29	77	100.0	36	15	Q79445	Q79445 human immun
30	77	100.0	37	15	Q80552	Q80552 human immun
31	77	100.0	41	15	Q77628	Q77628 human immun
32	77	100.0	42	15	Q77622	Q77622 human immun
33	77	100.0	42	15	Q77631	Q77631 human immun
34	77	100.0	42	15	Q77660	Q77660 human immun
35	77	100.0	42	15	Q77612	Q77612 human immun
36	77	100.0	42	15	Q77665	Q77665 human immun
37	77	100.0	42	15	Q77613	Q77613 human immun
38	77	100.0	42	15	Q77623	Q77623 human immun
39	77	100.0	42	15	Q77615	Q77615 human immun
40	77	100.0	42	15	Q77614	Q77614 human immun
41	77	100.0	45	15	Q97047	Q97047 human immun
42	77	100.0	46	15	Q97055	Q97055 human immun
43	77	100.0	55	15	O40263	O40263 human immun
44	77	100.0	56	15	O40267	O40267 human immun
45	77	100.0	57	15	Q97045	Q97045 human immun

ALIGNMENTS

RESULT 1
Q76740
ID Q76740 PRELIMINARY; PRT; 35 AA.
AC Q76740;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Env protein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NO.5;
RX MEDLINE=96296970; PubMed=8679313;
RA Kakizawa J., Ushijima H., Morishita Y., Oka S., Ikeda Y., Muller W.E.;
RT "Diversity of HIV type 1 envelope V3 loop region in saliva.";
RL AIDS Res. Hum. Retroviruses 12:561-563(1996).
DR EMBL; D78624; BAA11444.1; -.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1 1
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 3950 MW; 48994EA4990F0279 CRC64;

Query Match 100.0%; Score 77; DB 15; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
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Db 13 RIQRGPGRAFVTIGK 27

RESULT 2
Q76741
ID Q76741 PRELIMINARY; PRT; 35 AA.
AC Q76741;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

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DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Env protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NO.5;
RX   MEDLINE=96296970; PubMed=8679313;
RA   Kakizawa J., Ushijima H., Morishita Y., Oka S., Ikeda Y., Muller W.E.;
RT   "Diversity of HIV type 1 envelope V3 loop region in saliva.";
RL   AIDS Res. Hum. Retroviruses 12:561-563(1996).
DR   EMBL; D78625; BAA11445.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
FT   NON_TER      35     35
SQ   SEQUENCE   35 AA;  3950 MW;  48994EA4990F0279 CRC64;

  Query Match             100.0%;  Score 77;  DB 15;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db      13 RIQRGPGRAFVTIGK 27


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ID   Q79439      PRELIMINARY;      PRT;    35 AA.
AC   Q79439;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91240282; PubMed=2035026;
RA   Wain-Hobson S., Vartanian J.-P., Henry M., Chenciner N., Cheynier R.,
RA   Delassus S., Martins L.P., Sala M., Nugeyre M.-T., Guetard D.,
RA   Klatzmann D., Gluckman J.-C., Rozenbaum W., Barre-Sinoussi F.,
RA   Montagnier L.;
RT   "LAV revisited: Origins of the early viral HIV-1 isolates from
RT   Institut Pasteur.";
RL   Science 252:961-965(1991).
DR   EMBL; M64207; AAA44765.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   35 AA;  3939 MW;  A3DA68F9D10ADF1D CRC64;

  Query Match             100.0%;  Score 77;  DB 15;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db      12 RIQRGPGRAFVTIGK 26


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ID   Q80545      PRELIMINARY;      PRT;    36 AA.
AC   Q80545;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90364416; PubMed=2392685;
RA   LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant.";
RL   Science 249:932-935(1990).
DR   EMBL; M61582; AAA45268.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   36 AA;  4053 MW;  23A8994EA4990F02 CRC64;

  Query Match             100.0%;  Score 77;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db      13 RIQRGPGRAFVTIGK 27


RESULT 5
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AC   Q80546;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90364416; PubMed=2392685;
RA   LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant.";
RL   Science 249:932-935(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91118022; PubMed=1990444;
RA   LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant: Corrections and clarifications.";
RL   Science 251:811-811(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91361090; PubMed=1887238;
RA   LaRosa G.J., Weinhold K., Profy A.T., Langlois A.J., Dreesman G.R.,
RA   Boswell R.N., Shadduck P., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant: Further clarifications.";
RL   Science 253:1146-1146(1991).
DR   EMBL; M61584; AAA45269.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   36 AA;  4053 MW;  23A8994EA4990F02 CRC64;
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  Query Match             100.0%;  Score 77;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db     13 RIQRGPGRAFVTIGK 27


RESULT 6
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AC   Q80547;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90364416; PubMed=2392685;
RA   LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant.";
RL   Science 249:932-935(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91118022; PubMed=1990444;
RA   LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant: Corrections and clarifications.";
RL   Science 251:811-811(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91361090; PubMed=1887238;
RA   LaRosa G.J., Weinhold K., Profy A.T., Langlois A.J., Dreesman G.R.,
RA   Boswell R.N., Shadduck P., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant: Further clarifications.";
RL   Science 253:1146-1146(1991).
DR   EMBL; M61585; AAA45270.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   36 AA;  4053 MW;  23A8994EA4990F02 CRC64;

  Query Match             100.0%;  Score 77;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
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Qy      1 RIQRGPGRAFVTIGK 15
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Db     13 RIQRGPGRAFVTIGK 27


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AC   Q80548;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
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RX   MEDLINE=90364416; PubMed=2392685;
RA   LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant.";
RL   Science 249:932-935(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91118022; PubMed=1990444;
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RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant: Corrections and clarifications.";
RL   Science 251:811-811(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91361090; PubMed=1887238;
RA   LaRosa G.J., Weinhold K., Profy A.T., Langlois A.J., Dreesman G.R.,
RA   Boswell R.N., Shadduck P., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant: Further clarifications.";
RL   Science 253:1146-1146(1991).
DR   EMBL; M61586; AAA45271.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   36 AA;  4053 MW;  23A8994EA4990F02 CRC64;

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  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db     13 RIQRGPGRAFVTIGK 27


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AC   Q80549;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90364416; PubMed=2392685;
RA   LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant.";
RL   Science 249:932-935(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91118022; PubMed=1990444;
RA   LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
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RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant: Corrections and clarifications.";
RL   Science 251:811-811(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91361090; PubMed=1887238;
RA   LaRosa G.J., Weinhold K., Profy A.T., Langlois A.J., Dreesman G.R.,
RA   Boswell R.N., Shadduck P., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant: Further clarifications.";
RL   Science 253:1146-1146(1991).
DR   EMBL; M61587; AAA45272.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   36 AA;  4122 MW;  23A9895FA4990F02 CRC64;

  Query Match             100.0%;  Score 77;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
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Db      13 RIQRGPGRAFVTIGK 27


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DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90364416; PubMed=2392685;
RA   LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant.";
RL   Science 249:932-935(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91118022; PubMed=1990444;
RA   LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant: Corrections and clarifications.";
RL   Science 251:811-811(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91361090; PubMed=1887238;
RA   LaRosa G.J., Weinhold K., Profy A.T., Langlois A.J., Dreesman G.R.,
RA   Boswell R.N., Shadduck P., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant: Further clarifications.";
RL   Science 253:1146-1146(1991).
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KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   36 AA;  4193 MW;  62B118D6A4990F1E CRC64;

  Query Match             100.0%;  Score 77;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db      13 RIQRGPGRAFVTIGK 27


RESULT 10
Q80551
ID   Q80551      PRELIMINARY;      PRT;    36 AA.
AC   Q80551;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90364416; PubMed=2392685;
RA   LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant.";
RL   Science 249:932-935(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91118022; PubMed=1990444;
RA   LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
RA   Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shadduck P.,
RA   Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant: Corrections and clarifications.";
RL   Science 251:811-811(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91361090; PubMed=1887238;
RA   LaRosa G.J., Weinhold K., Profy A.T., Langlois A.J., Dreesman G.R.,
RA   Boswell R.N., Shadduck P., Bolognesi D.P., Matthews T.J., Emini E.A.,
RA   Putney S.D.;
RT   "Conserved sequence and structural elements in the HIV-1 principal
RT   neutralizing determinant: Further clarifications.";
RL   Science 253:1146-1146(1991).
DR   EMBL; M61589; AAA45274.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   36 AA;  4193 MW;  62B118D6A4990F1E CRC64;

  Query Match             100.0%;  Score 77;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db      13 RIQRGPGRAFVTIGK 27


RESULT 11
Q79428
ID   Q79428      PRELIMINARY;      PRT;    36 AA.
AC   Q79428;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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DE   Envelope protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91240282; PubMed=2035026;
RA   Wain-Hobson S., Vartanian J.-P., Henry M., Chenciner N., Cheynier R.,
RA   Delassus S., Martins L.P., Sala M., Nugeyre M.-T., Guetard D.,
RA   Klatzmann D., Gluckman J.-C., Rozenbaum W., Barre-Sinoussi F.,
RA   Montagnier L.;
RT   "LAV revisited: Origins of the early viral HIV-1 isolates from
RT   Institut Pasteur.";
RL   Science 252:961-965(1991).
DR   EMBL; M64186; AAA44754.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   36 AA;  4053 MW;  23A8994EA4990F02 CRC64;

  Query Match             100.0%;  Score 77;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db     13 RIQRGPGRAFVTIGK 27


RESULT 12
Q79429
ID   Q79429      PRELIMINARY;      PRT;    36 AA.
AC   Q79429;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91240282; PubMed=2035026;
RA   Wain-Hobson S., Vartanian J.-P., Henry M., Chenciner N., Cheynier R.,
RA   Delassus S., Martins L.P., Sala M., Nugeyre M.-T., Guetard D.,
RA   Klatzmann D., Gluckman J.-C., Rozenbaum W., Barre-Sinoussi F.,
RA   Montagnier L.;
RT   "LAV revisited: Origins of the early viral HIV-1 isolates from
RT   Institut Pasteur.";
RL   Science 252:961-965(1991).
DR   EMBL; M64187; AAA44755.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   36 AA;  4053 MW;  23A8994EA4990F02 CRC64;

  Query Match             100.0%;  Score 77;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db     13 RIQRGPGRAFVTIGK 27


RESULT 13
Q79430
ID   Q79430      PRELIMINARY;      PRT;    36 AA.
AC   Q79430;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91240282; PubMed=2035026;
RA   Wain-Hobson S., Vartanian J.-P., Henry M., Chenciner N., Cheynier R.,
RA   Delassus S., Martins L.P., Sala M., Nugeyre M.-T., Guetard D.,
RA   Klatzmann D., Gluckman J.-C., Rozenbaum W., Barre-Sinoussi F.,
RA   Montagnier L.;
RT   "LAV revisited: Origins of the early viral HIV-1 isolates from
RT   Institut Pasteur.";
RL   Science 252:961-965(1991).
DR   EMBL; M64188; AAA44756.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   36 AA;  4053 MW;  23A8994EA4990F02 CRC64;

  Query Match             100.0%;  Score 77;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db     13 RIQRGPGRAFVTIGK 27


RESULT 14
Q79433
ID   Q79433      PRELIMINARY;      PRT;    36 AA.
AC   Q79433;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope protein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91240282; PubMed=2035026;
RA   Wain-Hobson S., Vartanian J.-P., Henry M., Chenciner N., Cheynier R.,
RA   Delassus S., Martins L.P., Sala M., Nugeyre M.-T., Guetard D.,
RA   Klatzmann D., Gluckman J.-C., Rozenbaum W., Barre-Sinoussi F.,
RA   Montagnier L.;
RT   "LAV revisited: Origins of the early viral HIV-1 isolates from
RT   Institut Pasteur.";
RL   Science 252:961-965(1991).
DR   EMBL; M64190; AAA44759.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   36 AA;  4053 MW;  23A8994EA4990F02 CRC64;

  Query Match             100.0%;  Score 77;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db     13 RIQRGPGRAFVTIGK 27


RESULT 15
Q79415
ID   Q79415      PRELIMINARY;      PRT;    36 AA.
AC   Q79415;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope protein (Fragment).
GN   ENV.
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```
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91240282; PubMed=2035026;
RA   Wain-Hobson S., Vartanian J.-P., Henry M., Chenciner N., Cheynier R.,
RA   Delassus S., Martins L.P., Sala M., Nugeyre M.-T., Guetard D.,
RA   Klatzmann D., Gluckman J.-C., Rozenbaum W., Barre-Sinoussi F.,
RA   Montagnier L.;
RT   "LAV revisited: Origins of the early viral HIV-1 isolates from
RT   Institut Pasteur.";
RL   Science 252:961-965(1991).
DR   EMBL; M64194; AAA44741.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER       1      1
SQ   SEQUENCE   36 AA;  4152 MW;  62A8994EA4990F1E CRC64;

  Query Match             100.0%;  Score 77;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db      13 RIQRGPGRAFVTIGK 27


Search completed: March 10, 2003, 17:52:19
Job time : 31 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: March 10, 2003, 17:42:03 ; Search time 11 Seconds
(without alignments)
56.559 Million cell updates/sec

Title: US-09-191-772A-2
Perfect score: 77
Sequence: 1 RIQRGPGRAFVTIGK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	851	1	ENV_HV1B8	P04582 human immun
2	77	100.0	853	1	ENV_HV1MF	P19551 human immun
3	77	100.0	856	1	ENV_HV1B1	P03375 human immun
4	77	100.0	856	1	ENV_HV1H2	P04578 human immun
5	77	100.0	856	1	ENV_HV1H3	P04624 human immun
6	77	100.0	856	1	ENV_HV1PV	P03376 human immun
7	77	100.0	861	1	ENV_HV1BR	P03377 human immun
8	73	94.8	856	1	ENV_HV1LW	Q70626 human immun
9	45	58.4	848	1	ENV_HV1JR	P20871 human immun
10	44	57.1	852	1	ENV_HV1BN	P12488 human immun
11	44	57.1	856	1	ENV_HV1MN	P05877 human immun
12	44	57.1	867	1	ENV_HV1J3	P12489 human immun
13	43	55.8	855	1	ENV_HV1A2	P03378 human immun
14	43	55.8	861	1	ENV_HV1KB	P31819 human immun
15	43	55.8	1236	1	TOP2_LEICH	O61078 leishmania
16	42	54.5	855	1	ENV_HV1OY	P20888 human immun
17	41	53.2	1239	1	TOP2_CRIFA	P27570 crithidia f
18	40.5	52.6	894	1	SYLM_SACDO	P13503 saccharomyc
19	40	51.9	427	1	HISX_HAEIN	P44001 haemophilus
20	40	51.9	433	1	HISX_ECOLI	P06988 escherichia
21	40	51.9	433	1	HISX_SALTY	P10370 salmonella
22	40	51.9	868	1	ENV_HV1C4	P05879 human immun
23	39	50.6	843	1	ENV_HV1Y2	P35961 human immun
24	39	50.6	856	1	ENV_HV1SC	P05878 human immun
25	39	50.6	856	1	ENV_HV1W1	P31872 human immun
26	39	50.6	856	1	ENV_HV1ZH	P05881 human immun
27	39	50.6	879	1	RA50_SULTO	Q96yr5 sulfolobus
28	38	49.4	197	1	R16B_YEAST	P26785 saccharomyc
29	38	49.4	198	1	R16A_YEAST	P26784 saccharomyc
30	38	49.4	380	1	YH07_PASMU	Q9ckb7 pasteurella
31	38	49.4	441	1	MYCN_CHICK	P18444 gallus gall
32	38	49.4	655	1	IDUA_CANFA	Q01634 canis famil
33	38	49.4	847	1	ENV_HV1S1	P19550 human immun
34	38	49.4	852	1	ENV_HV1S3	P19549 human immun
35	37	48.1	334	1	PHP2_SCHPO	P24488 schizosacch
36	37	48.1	417	1	GLA3_PSEAE	Q9hvi7 pseudomonas
37	37	48.1	426	1	HISX_METTH	O26327 methanobact
38	37	48.1	435	1	HISX_BUCAI	P57201 buchnera ap
39	37	48.1	435	1	HISX_BUCAP	Q9zhe6 buchnera ap
40	37	48.1	473	1	L14B_LITER	Q40153 lithospermu
41	37	48.1	475	1	L14B_PRUAR	O24467 prunus arme
42	37	48.1	687	1	SRB4_YEAST	P32569 saccharomyc
43	37	48.1	795	1	HIS2_KLULA	O13471 kluyveromyc
44	37	48.1	799	1	HIS2_SACBA	Q12670 saccharomyc
45	37	48.1	799	1	HIS2_YEAST	P00815 saccharomyc

ALIGNMENTS

RESULT 1
ENV_HV1B8
ID ENV_HV1B8 STANDARD; PRT; 851 AA.
AC P04582;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11684;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).
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DR EMBL; K02011; AAA44661.1; -.
DR HIV; K02011; ENV$BH8.
DR GlycoSuiteDB; P04582; -.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 507 851 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 440 BY SIMILARITY.
FT DISULFID 385 413 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT   CARBOHYD    156    156       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    160    160       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    230    230       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    234    234       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    241    241       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    262    262       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    276    276       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    301    301       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    332    332       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    339    339       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    356    356       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    386    386       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    392    392       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    401    401       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    443    443       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    458    458       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    606    606       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    611    611       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    620    620       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    632    632       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    669    669       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    745    745       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    811    811       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   851 AA;  96644 MW;  D16A3C90857785F1 CRC64;

  Query Match             100.0%;  Score 77;  DB 1;  Length 851;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db     308 RIQRGPGRAFVTIGK 322


RESULT 2
ENV_HV1MF
ID   ENV_HV1MF      STANDARD;      PRT;   853 AA.
AC   P19551;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11704;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90317877; PubMed=1695254;
RA   Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier C.,
RA   Wasiak A.;
RT   "Cloning and characterization of human immunodeficiency virus type 1
RT   variants diminished in the ability to induce syncytium-independent
RT   cytolysis.";
RL   J. Virol. 64:3792-3803(1990).
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M33943; AAA44850.1; -.
DR   HIV; M33943; ENV$MFA.
DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL        1     30
FT   CHAIN        31    509       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN       510    853       TRANSMEMBRANE GLYCOPROTEIN.
FT   DISULFID     54     74       BY SIMILARITY.
FT   DISULFID    119    203       BY SIMILARITY.
FT   DISULFID    126    194       BY SIMILARITY.
FT   DISULFID    131    157       BY SIMILARITY.
FT   DISULFID    216    245       BY SIMILARITY.
FT   DISULFID    226    237       BY SIMILARITY.
FT   DISULFID    294    329       BY SIMILARITY.
FT   DISULFID    376    443       BY SIMILARITY.
FT   DISULFID    383    416       BY SIMILARITY.
FT   CARBOHYD     88     88       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    136    136       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    156    156       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    160    160       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    195    195       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    232    232       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    239    239       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    260    260       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    274    274       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    287    287       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    293    293       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    299    299       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    330    330       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    354    354       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    384    384       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    390    390       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    395    395       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    404    404       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    446    446       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    461    461       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    609    609       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    614    614       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    623    623       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    635    635       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    672    672       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    748    748       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    814    814       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   853 AA;  96912 MW;  3377B993B6F22ABA CRC64;

  Query Match             100.0%;  Score 77;  DB 1;  Length 853;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db     306 RIQRGPGRAFVTIGK 320


RESULT 3
ENV_HV1B1
ID   ENV_HV1B1      STANDARD;      PRT;   856 AA.
AC   P03375;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11678;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85111123; PubMed=2578615;
RA   Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA   Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
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RA   Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA   Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,
RA   Wong-Staal F.;
RT   "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL   Nature 313:277-284(1985).
RN   [2]
RP   DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX   MEDLINE=90285159; PubMed=2355006;
RA   Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA   Gregory T.J.;
RT   "Assignment of intrachain disulfide bonds and characterization of
RT   potential glycosylation sites of the type 1 recombinant human
RT   immunodeficiency virus envelope glycoprotein (gp120) expressed in
RT   Chinese hamster ovary cells.";
RL   J. Biol. Chem. 265:10373-10382(1990).
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M15654; AAA44205.1; -.
DR   PIR; A03973; VCLJH3.
DR   HIV; M15654; ENV$BH102.
DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL       1    30
FT   CHAIN       31   511       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN      512   856       TRANSMEMBRANE GLYCOPROTEIN.
FT   DISULFID    54    74
FT   DISULFID   119   205
FT   DISULFID   126   196
FT   DISULFID   131   157
FT   DISULFID   218   247
FT   DISULFID   228   239
FT   DISULFID   296   331
FT   DISULFID   378   445
FT   DISULFID   385   418
FT   CARBOHYD    88    88       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   136   136       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   141   141       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   156   156       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   160   160       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   186   186       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   197   197       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   230   230       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   234   234       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   241   241       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   262   262       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   276   276       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   289   289       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   295   295       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   301   301       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   332   332       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   339   339       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   356   356       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   386   386       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   392   392       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   397   397       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   406   406       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   448   448       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   463   463       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   611   611       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   616   616       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   625   625       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   637   637       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   674   674       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   750   750       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   816   816       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   856 AA;  97224 MW;  0BFFB1A18931BB27 CRC64;

  Query Match             100.0%;  Score 77;  DB 1;  Length 856;
  Best Local Similarity   100.0%;  Pred. No. 4e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db     308 RIQRGPGRAFVTIGK 322


RESULT 4
ENV_HV1H2
ID   ENV_HV1H2      STANDARD;      PRT;   856 AA.
AC   P04578; O09779;
DT   13-AUG-1987 (Rel. 05, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11706;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87299196; PubMed=3040055;
RA   Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA   Gallo R.C., Wong-Staal F.;
RT   "Complete nucleotide sequences of functional clones of the AIDS
RT   virus.";
RL   AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN   [2]
RP   REVISIONS.
RA   Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA   Gallo R.C., Wong-Staal F.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K03455; AAB50262.1; -.
DR   EMBL; AF038399; AAB99976.1; -.
DR   EMBL; AF033819; AAC82596.1; -.
DR   HIV; K03455; ENV$HXB2.
DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL       1    30
FT   CHAIN       31   511       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN      512   856       TRANSMEMBRANE GLYCOPROTEIN.
FT   DISULFID    54    74       BY SIMILARITY.
FT   DISULFID   119   205       BY SIMILARITY.
FT   DISULFID   126   196       BY SIMILARITY.
FT   DISULFID   131   157       BY SIMILARITY.
FT   DISULFID   218   247       BY SIMILARITY.
FT   DISULFID   228   239       BY SIMILARITY.
FT   DISULFID   296   331       BY SIMILARITY.
FT   DISULFID   378   445       BY SIMILARITY.
FT   DISULFID   385   418       BY SIMILARITY.
FT   CARBOHYD    88    88       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   136   136       N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    156    156       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    160    160       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    230    230       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    234    234       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    241    241       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    262    262       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    276    276       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    301    301       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    332    332       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    339    339       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    356    356       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    386    386       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    392    392       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    397    397       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    406    406       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    448    448       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    463    463       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    611    611       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    616    616       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    624    624       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    637    637       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    674    674       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    750    750       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    816    816       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   856 AA;  97212 MW;  6FAB16AF85107FE0 CRC64;

  Query Match             100.0%;  Score 77;  DB 1;  Length 856;
  Best Local Similarity   100.0%;  Pred. No. 4e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           ||||||||||||||||
Db     308 RIQRGPGRAFVTIGK 322


RESULT 5
ENV_HV1H3
ID   ENV_HV1H3      STANDARD;      PRT;   856 AA.
AC   P04624;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11707;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85228248; PubMed=2988795;
RA   Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
RA   Shaw G.M., Wong-Staal F., Reddy E.P.;
RT   "HTLV-III env gene products synthesized in E. coli are recognized by
RT   antibodies present in the sera of AIDS patients.";
RL   Cell 41:979-986(1985).
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14100; AAA44679.1; -.
DR   HIV; M14100; ENV$HXB3.
DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL        1     30
FT   CHAIN        31    511       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN       512    856       TRANSMEMBRANE GLYCOPROTEIN.
FT   DISULFID    119    205       BY SIMILARITY.
FT   DISULFID    126    196       BY SIMILARITY.
FT   DISULFID    131    157       BY SIMILARITY.
FT   DISULFID    218    247       BY SIMILARITY.
FT   DISULFID    228    239       BY SIMILARITY.
FT   DISULFID    296    331       BY SIMILARITY.
FT   DISULFID    378    445       BY SIMILARITY.
FT   DISULFID    385    418       BY SIMILARITY.
FT   CARBOHYD     88     88       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    136    136       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    156    156       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    160    160       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    230    230       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    234    234       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    241    241       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    262    262       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    276    276       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    301    301       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    332    332       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    339    339       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    356    356       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    386    386       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    392    392       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    397    397       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    406    406       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    448    448       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    463    463       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    611    611       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    616    616       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    624    624       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    637    637       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    674    674       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    750    750       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    816    816       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   856 AA;  97188 MW;  3373C68BB84C1AFC CRC64;

  Query Match             100.0%;  Score 77;  DB 1;  Length 856;
  Best Local Similarity   100.0%;  Pred. No. 4e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           ||||||||||||||||
Db     308 RIQRGPGRAFVTIGK 322


RESULT 6
ENV_HV1PV
ID   ENV_HV1PV      STANDARD;      PRT;   856 AA.
AC   P03376;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11700;
RN   [1]
RP   SEQUENCE FROM N.A.
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RX   MEDLINE=85111157; PubMed=2982104;
RA   Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA   Capon D.J.;
RT   "Nucleic acid structure and expression of the human
RT   AIDS/lymphadenopathy retrovirus.";
RL   Nature 313:450-458(1985).
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K02083; AAB59873.1; -.
DR   EMBL; X01762; CAA25903.1; ALT_SEQ.
DR   PIR; A03974; VCLJVL.
DR   HIV; K02083; ENV$PV22.
DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL        1     30
FT   CHAIN        31    511       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN       512    856       TRANSMEMBRANE GLYCOPROTEIN.
FT   DISULFID     54     74       BY SIMILARITY.
FT   DISULFID    119    205       BY SIMILARITY.
FT   DISULFID    126    196       BY SIMILARITY.
FT   DISULFID    131    157       BY SIMILARITY.
FT   DISULFID    218    247       BY SIMILARITY.
FT   DISULFID    228    239       BY SIMILARITY.
FT   DISULFID    296    331       BY SIMILARITY.
FT   DISULFID    378    445       BY SIMILARITY.
FT   DISULFID    385    418       BY SIMILARITY.
FT   CARBOHYD     88     88       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    136    136       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    156    156       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    160    160       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    230    230       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    234    234       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    241    241       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    262    262       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    276    276       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    301    301       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    332    332       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    339    339       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    356    356       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    386    386       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    392    392       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    397    397       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    406    406       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    448    448       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    463    463       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    611    611       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    616    616       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    625    625       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    637    637       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    674    674       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    750    750       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    816    816       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   856 AA;  97339 MW;  5FCDB1DC3C1209B3 CRC64;

  Query Match           100.0%;  Score 77;  DB 1;  Length 856;
  Best Local Similarity  100.0%;  Pred. No. 4e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db     308 RIQRGPGRAFVTIGK 322


RESULT 7
ENV_HV1BR
ID   ENV_HV1BR      STANDARD;      PRT;   861 AA.
AC   P03377;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11686;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099333; PubMed=2981635;
RA   Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
RT   "Nucleotide sequence of the AIDS virus, LAV.";
RL   Cell 40:9-17(1985).
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K02013; AAB59751.1; -.
DR   EMBL; A04321; CAA00352.1; -.
DR   PIR; A03975; VCLJLV.
DR   HIV; K02013; ENV$BRU.
DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL        1     30
FT   CHAIN        31    516       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN       517    861       TRANSMEMBRANE GLYCOPROTEIN.
FT   DISULFID     54     74       BY SIMILARITY.
FT   DISULFID    119    210       BY SIMILARITY.
FT   DISULFID    126    201       BY SIMILARITY.
FT   DISULFID    131    162       BY SIMILARITY.
FT   DISULFID    223    252       BY SIMILARITY.
FT   DISULFID    233    244       BY SIMILARITY.
FT   DISULFID    301    336       BY SIMILARITY.
FT   DISULFID    383    450       BY SIMILARITY.
FT   DISULFID    390    423       BY SIMILARITY.
FT   CARBOHYD     88     88       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    136    136       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    146    146       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    191    191       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    202    202       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    235    235       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    239    239       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    246    246       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    267    267       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    281    281       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    294    294       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    300    300       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    306    306       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    337    337       N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT   CARBOHYD    344    344       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    361    361       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    391    391       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    397    397       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    402    402       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    411    411       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    453    453       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    468    468       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    616    616       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    621    621       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    630    630       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    642    642       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    679    679       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    755    755       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    821    821       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   861 AA;  97487 MW;  04DE2B4D4E4FD63A CRC64;

  Query Match             100.0%;  Score 77;  DB 1;  Length 861;
  Best Local Similarity   100.0%;  Pred. No. 4e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db     313 RIQRGPGRAFVTIGK 327


RESULT 8
ENV_HV1LW
ID   ENV_HV1LW      STANDARD;      PRT;   856 AA.
AC   Q70626;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (LW12.3 isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=82834;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95127297; PubMed=7826699;
RA   Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
RA   Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT   "Viral variability and serum antibody response in a laboratory worker
RT   infected with HIV type 1 (HTLV type IIIB).";
RL   AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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CC   ---------------------------------------------------------------------
DR   EMBL; U12055; AAA76690.1; -.
DR   GlycoSuiteDB; Q70626; -.
DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL       1     30
FT   CHAIN       31    511       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN      512    856       TRANSMEMBRANE GLYCOPROTEIN.
FT   DISULFID    54     74       BY SIMILARITY.
FT   DISULFID   119    205       BY SIMILARITY.
FT   DISULFID   126    196       BY SIMILARITY.
FT   DISULFID   131    157       BY SIMILARITY.
FT   DISULFID   218    247       BY SIMILARITY.
FT   DISULFID   228    239       BY SIMILARITY.
FT   DISULFID   296    331       BY SIMILARITY.
FT   DISULFID   378    445       BY SIMILARITY.
FT   DISULFID   385    418       BY SIMILARITY.
FT   CARBOHYD    88     88       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   136    136       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   156    156       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   160    160       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   230    230       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   234    234       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   241    241       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   262    262       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   276    276       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   301    301       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   332    332       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   339    339       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   356    356       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   386    386       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   392    392       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   397    397       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   406    406       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   448    448       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   463    463       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   611    611       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   616    616       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   624    624       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   637    637       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   674    674       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   750    750       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   816    816       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   856 AA;  96938 MW;  0C241332CF7E6687 CRC64;

  Query Match             94.8%;  Score 73;  DB 1;  Length 856;
  Best Local Similarity   93.3%;  Pred. No. 2.1e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||| ||||||
Db     308 RIQRGPGRTFVTIGK 322


RESULT 9
ENV_HV1JR
ID   ENV_HV1JR      STANDARD;      PRT;   848 AA.
AC   P20871;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11688;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Koyanagi S., Chen I.S.Y.;
RL   Submitted (DEC-1988) to the HIV data bank.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M38429; AAB03749.1; -.
DR   HIV; M38429; ENV$JRCSF.
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DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL        1     32
FT   CHAIN        33    503       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN       504    848       TRANSMEMBRANE GLYCOPROTEIN.
FT   DISULFID     53     73       BY SIMILARITY.
FT   DISULFID    118    203       BY SIMILARITY.
FT   DISULFID    125    194       BY SIMILARITY.
FT   DISULFID    130    154       BY SIMILARITY.
FT   DISULFID    216    245       BY SIMILARITY.
FT   DISULFID    226    237       BY SIMILARITY.
FT   DISULFID    294    328       BY SIMILARITY.
FT   DISULFID    374    437       BY SIMILARITY.
FT   DISULFID    381    410       BY SIMILARITY.
FT   CARBOHYD     87     87       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    134    134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    137    137       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    153    153       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    157    157       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    185    185       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    195    195       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    228    228       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    239    239       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    260    260       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    274    274       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    287    287       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    293    293       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    299    299       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    329    329       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    336    336       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    352    352       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    382    382       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    388    388       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    392    392       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    403    403       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    440    440       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    453    453       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    603    603       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    608    608       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    617    617       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    629    629       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    808    808       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   848 AA;  96475 MW;  20767F51227EC3F3 CRC64;

  Query Match             58.4%;  Score 45;  DB 1;  Length 848;
  Best Local Similarity   64.3%;  Pred. No. 2.5;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 IQRGPGRAFVTIGK 15
          |  ||||||  | |:
Db    305 IHIGPGRAFYTTGE 318


RESULT 10
ENV_HV1BN
ID   ENV_HV1BN      STANDARD;      PRT;   852 AA.
AC   P12488;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11693;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89085613; PubMed=2789516;
RA   Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,
RA   Dandekar S.;
RT   "Biological and molecular characterization of human immunodeficiency
RT   virus (HIV-1BR) from the brain of a patient with progressive
RT   dementia.";
RL   Virology 168:79-39(1989).
CC   -!- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
CC       HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; M21098; AAA44221.1; -.
DR   PIR; A31667; VCLJBR.
DR   HIV; M21098; ENV$BRVA.
DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL        1     30
FT   CHAIN        31    507       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN       508    852       TRANSMEMBRANE GLYCOPROTEIN.
FT   DISULFID     54     74       BY SIMILARITY.
FT   DISULFID    119    205       BY SIMILARITY.
FT   DISULFID    126    196       BY SIMILARITY.
FT   DISULFID    131    155       BY SIMILARITY.
FT   DISULFID    218    247       BY SIMILARITY.
FT   DISULFID    228    239       BY SIMILARITY.
FT   DISULFID    296    330       BY SIMILARITY.
FT   DISULFID    376    439       BY SIMILARITY.
FT   DISULFID    383    412       BY SIMILARITY.
FT   CARBOHYD     49     49       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     88     88       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    138    138       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    154    154       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    158    158       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    234    234       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    241    241       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    262    262       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    276    276       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    301    301       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    331    331       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    354    354       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    360    360       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    384    384       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    390    390       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    396    396       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    400    400       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    442    442       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    456    456       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    607    607       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    612    612       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    621    621       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    633    633       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    670    670       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    812    812       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   852 AA;  97203 MW;  2BB866345DEC915F CRC64;

  Query Match             57.1%;  Score 44;  DB 1;  Length 852;
  Best Local Similarity   53.3%;  Pred. No. 3.8;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;
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Qy       1 RIQRGPGRAFVTIGK 15
           ||  |||| : | |:
Db     306 RITMGPGRVYYTTGQ 320


RESULT 11
ENV_HV1MN
ID   ENV_HV1MN      STANDARD;      PRT;   856 AA.
AC   P05877;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11696;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88219542; PubMed=3369091;
RA   Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA   Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT   "Envelope sequences of two new United States HIV-1 isolates.";
RL   Virology 164:531-536(1988).
CC   -!- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC       PATIENT IN 1984.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M17449; AAA44857.1; -.
DR   PIR; A28922; VCLJMN.
DR   HIV; M17449; ENV$MN.
DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL        1     29
FT   CHAIN        30    513       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN       514    856       TRANSMEMBRANE GLYCOPROTEIN.
FT   DISULFID     53     73       BY SIMILARITY.
FT   DISULFID    118    210       BY SIMILARITY.
FT   DISULFID    125    201       BY SIMILARITY.
FT   DISULFID    130    162       BY SIMILARITY.
FT   DISULFID    223    252       BY SIMILARITY.
FT   DISULFID    233    244       BY SIMILARITY.
FT   DISULFID    301    335       BY SIMILARITY.
FT   DISULFID    381    445       BY SIMILARITY.
FT   DISULFID    388    418       BY SIMILARITY.
FT   CARBOHYD     87     87       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    129    129       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    140    140       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    146    146       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    191    191       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    202    202       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    246    246       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    267    267       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    281    281       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    294    294       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    300    300       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    336    336       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    343    343       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    359    359       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    365    365       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    395    395       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    401    401       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    405    405       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    406    406       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    413    413       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    448    448       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    465    465       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    612    612       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    617    617       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    626    626       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    638    638       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    816    816       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   856 AA;  97140 MW;  D197D809940BE732 CRC64;

  Query Match             57.1%;  Score 44;  DB 1;  Length 856;
  Best Local Similarity   75.0%;  Pred. No. 3.8;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVT 12
           ||  |||||| |
Db     311 RIHIGPGRAFYT 322


RESULT 12
ENV_HV1J3
ID   ENV_HV1J3      STANDARD;      PRT;   867 AA.
AC   P12489;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11694;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89352108; PubMed=2669897;
RA   Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
RT   "Nucleotide sequences of gag and env genes of a Japanese isolate of
RT   HIV-1 and their expression in bacteria.";
RL   AIDS Res. Hum. Retroviruses 5:411-419(1989).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M21138; AAB03526.1; -.
DR   HIV; M21138; ENV$JH3.
DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL        1     30
FT   CHAIN        31    516       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN       517    867       TRANSMEMBRANE GLYCOPROTEIN.
FT   DISULFID     53     73       BY SIMILARITY.
FT   DISULFID    118    217       BY SIMILARITY.
FT   DISULFID    125    208       BY SIMILARITY.
FT   DISULFID    130    160       BY SIMILARITY.
FT   DISULFID    230    259       BY SIMILARITY.
FT   DISULFID    240    251       BY SIMILARITY.
FT   DISULFID    308    342       BY SIMILARITY.
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FT   DISULFID    388    457       BY SIMILARITY.
FT   DISULFID    395    430       BY SIMILARITY.
FT   CARBOHYD     87     87       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    140    140       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    143    143       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    159    159       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    188    188       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    189    189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    199    199       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    209    209       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    246    246       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    253    253       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    274    274       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    288    288       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    307    307       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    350    350       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    366    366       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    372    372       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    396    396       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    402    402       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    408    408       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    412    412       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    418    418       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    423    423       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    460    460       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    475    475       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    622    622       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    627    627       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    636    636       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    648    648       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   867 AA;  98399 MW;  5F2310146B8E8680 CRC64;

  Query Match             57.1%;  Score 44;  DB 1;  Length 867;
  Best Local Similarity   75.0%;  Pred. No. 3.9;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVT 12
          ||  |||||| |
Db    318 RIHIGPGRAFYT 329


RESULT 13
ENV_HV1A2
ID   ENV_HV1A2      STANDARD;      PRT;   855 AA.
AC   P03378;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN   ENV.
OS   Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85090453; PubMed=2578227;
RA   Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
RA   Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
RA   Levy J.A., Dina D., Luciw P.A.;
RT   "Nucleotide sequence and expression of an AIDS-associated retrovirus
RT   (ARV-2).";
RL   Science 227:484-492(1985).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K02007; AAB59882.1; -.
DR   PIR; A03976; VCLJA2.
DR   HIV; K02007; ENV$SP2.
DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL        1     29
FT   CHAIN        30    509       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN       510    855       TRANSMEMBRANE GLYCOPROTEIN.
FT   DISULFID     53     73       BY SIMILARITY.
FT   DISULFID    118    208       BY SIMILARITY.
FT   DISULFID    125    199       BY SIMILARITY.
FT   DISULFID    130    155       BY SIMILARITY.
FT   DISULFID    221    250       BY SIMILARITY.
FT   DISULFID    231    242       BY SIMILARITY.
FT   DISULFID    299    333       BY SIMILARITY.
FT   DISULFID    380    442       BY SIMILARITY.
FT   DISULFID    387    415       BY SIMILARITY.
FT   CARBOHYD     87     87       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    129    129       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    140    140       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    154    154       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    158    158       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    184    184       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    190    190       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    200    200       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    233    233       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    244    244       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    265    265       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    279    279       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    292    292       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    298    298       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    304    304       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    334    334       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    341    341       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    358    358       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    364    364       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    388    388       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    394    394       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    400    400       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    408    408       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    445    445       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    458    458       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    461    461       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    610    610       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    615    615       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    624    624       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    636    636       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    815    815       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   855 AA;  97438 MW;  A3BC20573AAC41A2 CRC64;

  Query Match             55.8%;  Score 43;  DB 1;  Length 855;
  Best Local Similarity   72.7%;  Pred. No. 5.8;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      5 GPGRAFVTIGK 15
          |||||| | |:
Db    313 GPGRAFHTTGR 323


RESULT 14
ENV_HV1KB
ID   ENV_HV1KB      STANDARD;      PRT;   861 AA.
AC   P31819;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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GN   ENV.
OS   Human immunodeficiency virus type 1 (KB-1 isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=36375;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92351552; PubMed=1322587;
RA   Shimizu H., Hasebe F., Tsuchie H., Morikawa S., Ushijima H.,
RA   Kitamura T.;
RT   "Analysis of a human immunodeficiency virus type 1 isolate carrying a
RT   truncated transmembrane glycoprotein.";
RL   Virology 189:534-546(1992).
CC   -!- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN
CC       THE CODONS FOR 729-ALA AND 730-ARG.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D12582; BAA02124.1; ALT_SEQ.
DR   PIR; A42995; VCLJKB.
DR   PIR; B42995; VCLJKX.
DR   InterPro; IPR000328; Env_GP41.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
DR   Pfam; PF00517; GP41; 1.
KW   AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW   Signal.
FT   SIGNAL       1     35       POTENTIAL.
FT   CHAIN       36    517       EXTERIOR MEMBRANE GLYCOPROTEIN.
FT   CHAIN      518    861       TRANSMEMBRANE GLYCOPROTEIN.
FT   TRANSMEM   690    711       POTENTIAL.
FT   DISULFID    59     79       BY SIMILARITY.
FT   DISULFID   124    212       BY SIMILARITY.
FT   DISULFID   131    203       BY SIMILARITY.
FT   DISULFID   136    160       BY SIMILARITY.
FT   DISULFID   225    254       BY SIMILARITY.
FT   DISULFID   235    246       BY SIMILARITY.
FT   DISULFID   303    337       BY SIMILARITY.
FT   DISULFID   383    446       BY SIMILARITY.
FT   DISULFID   390    419       BY SIMILARITY.
FT   CARBOHYD    93     93       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   145    145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   146    146       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   159    159       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   191    191       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   192    192       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   237    237       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   241    241       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   269    269       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   283    283       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   296    296       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   308    308       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   338    338       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   345    345       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   361    361       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   367    367       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   397    397       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   403    403       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   408    408       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   414    414       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   449    449       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   465    465       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   468    468       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   617    617       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   622    622       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   631    631       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   643    643       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   821    821       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   861 AA;  98116 MW;  3C06787658F0C9DA CRC64;

  Query Match             55.8%;  Score 43;  DB 1;  Length 861;
  Best Local Similarity   46.7%;  Pred. No. 5.9;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |:  |||| : | |:
Db     313 RVTMGPGRVYYTTGE 327


RESULT 15
TOP2_LEICH
ID   TOP2_LEICH     STANDARD;      PRT;  1236 AA.
AC   O61078;
DT   15-DEC-1998 (Rel. 37, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   DNA topoisomerase II (EC 5.99.1.3).
GN   TOP2.
OS   Leishmania chagasi.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=44271;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MHOM/BR/86/L669;
RA   Tepe-Lansdell T., Mann B.J., Labombard M., Macdonald T., Slunt K.M.,
RA   Pearson R.D.;
RT   "Isolation of a gene encoding a DNA topoisomerase II of Leishmania
RT   (Leishmania) chagasi.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
CC       BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
CC       MAKES DOUBLE-STRAND BREAKS.
CC   -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC       of double-stranded DNA.
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
CC       NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
CC       RELAX ONLY NEGATIVE SUPERCOILS.
CC   -!- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF051307; AAC05295.2; -.
DR   HSSP; P06786; 1BGW.
DR   InterPro; IPR003594; ATPbind_ATPase.
DR   InterPro; IPR001241; DNA_topoisoII.
DR   InterPro; IPR002205; DNA_topoisoIV.
DR   Pfam; PF00204; DNA_gyraseB; 1.
DR   Pfam; PF00521; DNA_topoisoIV; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   PRINTS; PR00418; TPI2FAMILY.
DR   ProDom; PD000616; DNA_topoisoII; 1.
DR   ProDom; PD000742; DNA_topoisoIV; 1.
DR   SMART; SM00387; HATPase_c; 1.
DR   SMART; SM00433; TOP2c; 1.
DR   SMART; SM00434; TOP4c; 1.
DR   PROSITE; PS00177; TOPOISOMERASE_II; 1.
KW   Isomerase; Topoisomerase; ATP-binding.
FT   NP_BIND     137    142       ATP (POTENTIAL).
FT   ACT_SITE    775    775       DNA CLEAVAGE (BY SIMILARITY).
SQ   SEQUENCE   1236 AA;  138968 MW;  A3209B95A078045C CRC64;
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Query Match 55.8%; Score 43; DB 1; Length 1236;
Best Local Similarity 42.9%; Pred. No. 8.5;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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Qy       2 IQRGPGRAFVTIGK 15
           ::|||    |: :||
Db     873 VRRGPDNEFIAVGK 886
```

Search completed: March 10, 2003, 17:51:36
Job time : 12 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: March 10, 2003, 17:45:18 ; Search time 21 Seconds
(without alignments)
68.667 Million cell updates/sec

Title: US-09-191-772A-2
Perfect score: 77
Sequence: 1 RIQRGPGRAFVTIGK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	851	2	S33985	env polyprotein -
2	77	100.0	854	2	S13288	env protein - huma
3	77	100.0	856	1	VCLJH3	env polyprotein pr
4	77	100.0	856	1	VCLJVL	env polyprotein pr
5	77	100.0	861	1	VCLJLV	env polyprotein pr
6	60	77.9	20	2	S65399	immunodeficiency v
7	52	67.5	861	1	VCLJSC	env polyprotein pr
8	47	61.0	35	2	PC2296	V3 domain peptide
9	45	58.4	35	2	PC2295	V3 domain peptide
10	45	58.4	77	2	S35809	envelope protein -
11	45	58.4	77	2	S35808	envelope protein -
12	45	58.4	77	2	S35848	envelope protein -
13	45	58.4	77	2	S35815	envelope protein -
14	45	58.4	77	2	S35849	envelope protein -
15	45	58.4	77	2	S35861	envelope protein -
16	45	58.4	77	2	S35862	envelope protein -
17	45	58.4	110	2	A46410	envelope protein (
18	45	58.4	110	2	D46410	envelope protein (
19	45	58.4	443	2	C41621	env polyprotein P
20	45	58.4	685	2	B82606	conjugal transfer
21	45	58.4	847	2	T09448	envelope glycoprot
22	45	58.4	847	2	S13289	env protein - huma
23	44	57.1	77	2	S35807	envelope protein -
24	44	57.1	77	2	S35816	envelope protein -
25	44	57.1	445	2	A41621	env polyprotein M
26	44	57.1	454	2	B41621	env polyprotein D
27	44	57.1	687	2	T08528	probable DNA topoi
28	44	57.1	852	1	VCLJBR	env polyprotein -
29	44	57.1	859	1	VCLJMN	env polyprotein pr
30	43	55.8	76	2	S35859	envelope protein -
31	43	55.8	77	2	S35858	envelope protein -
32	43	55.8	77	2	S35821	envelope protein -
33	43	55.8	77	2	S35857	envelope protein -
34	43	55.8	77	2	S35819	envelope protein -
35	43	55.8	77	2	S35820	envelope protein -
36	43	55.8	729	1	VCLJKX	env polyprotein pr
37	43	55.8	812	2	T48016	probable zinc-fing
38	43	55.8	855	1	VCLJA2	env polyprotein pr
39	43	55.8	861	1	VCLJKB	env polyprotein pr
40	42	54.5	71	2	S42918	env polyprotein -
41	42	54.5	316	2	H90372	catechol 2,3-dioxy
42	41	53.2	71	2	S42904	env polyprotein -
43	41	53.2	71	2	S42905	env polyprotein -
44	41	53.2	77	2	S35835	envelope protein -
45	41	53.2	77	2	S35836	envelope protein -

ALIGNMENTS

RESULT 1
S33985
env polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C;Accession: S33985
R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Accession: S33985
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-851 <CAR>
A;Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199
C;Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 77; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db     308 RIQRGPGRAFVTIGK 322
```

RESULT 2
S13288
env protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S13288
R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 c
A;Reference number: S13288; MUID:91043044; PMID:2172833
A;Accession: S13288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-854 <OBR>
C;Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 77; DB 2; Length 854;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db     306 RIQRGPGRAFVTIGK 320
```

RESULT 3
VCLJH3

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03973
R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora
nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A;Reference number: A93353; MUID:85111123; PMID:2578615
A;Accession: A03973
A;Molecule type: DNA
A;Residues: 1-856 <RAT>
A;Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic

  Query Match 100.0%; Score 77; DB 1; Length 856;
  Best Local Similarity 100.0%; Pred. No. 2.6e-05;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
|||||||||||||||
Db 308 RIQRGPGRAFVTIGK 322

RESULT 4
VCLJVL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03974
R;Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi
A;Reference number: A93355; MUID:85111157; PMID:2982104
A;Accession: A03974
A;Molecule type: DNA
A;Residues: 1-856 <MUE>
A;Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic

  Query Match 100.0%; Score 77; DB 1; Length 856;
  Best Local Similarity 100.0%; Pred. No. 2.6e-05;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
|||||||||||||||
Db 308 RIQRGPGRAFVTIGK 322

RESULT 5
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03975
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A03975
A;Molecule type: DNA
A;Residues: 1-861 <WAI>
A;Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F;517-861/Product: transmembrane glycoprotein #status predicted <TMM>
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predict

  Query Match 100.0%; Score 77; DB 1; Length 861;
  Best Local Similarity 100.0%; Pred. No. 2.6e-05;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
|||||||||||||||
Db 313 RIQRGPGRAFVTIGK 327

RESULT 6
S65399
immunodeficiency virus type 1, HIV-1 gp120 - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S65399
R;Niwa, Y.; Yano, M.; Futaki, S.; Okumura, Y.; Kido, H.
Eur. J. Biochem. 237, 64-70, 1996
A;Title: T-cell membrane-associated serine protease, tryptase TL(2), binds human immunode
man immunodeficiency virus type 1 inhibit cleavage of gp120.
A;Reference number: S65399; MUID:96203909; PMID:8620895
A;Accession: S65399
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10;11-20 <NIW>
C;Superfamily: type E retrovirus env polyprotein

  Query Match 77.9%; Score 60; DB 2; Length 20;
  Best Local Similarity 91.7%; Pred. No. 0.00073;
  Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RGPGRAFVTIGK 15
|||||||||||:
Db 1 RGPGRAFVTIGR 12

RESULT 7
VCLJSC
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C;Accession: B28922
R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Staa
Virology 164, 531-536, 1988
A;Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3369091
A;Accession: B28922
A;Molecule type: DNA
A;Residues: 1-861 <GUR>
C;Genetics:

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A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-861/Product: env polyprotein #status predicted <EPP>
F;87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

  Query Match             67.5%;  Score 52;  DB 1;  Length 861;
  Best Local Similarity   76.9%;  Pred. No. 0.58;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 IQRGPGRAFVTIG 14
          |||||||||   |
Db    309 IQRGPGRAFYATG 321


RESULT 8
PC2296
V3 domain peptide P4346 - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 07-May-1999
C;Accession: PC2296
R;Sherefa, K.; Soennerborg, A.; Steinbergs, J.; Saellberg, M.
Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994
A;Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping a
A;Reference number: PC2291; MUID:95110306; PMID:7811250
A;Accession: PC2296
A;Molecule type: protein
A;Residues: 1-35 <SHE>
C;Superfamily: type E retrovirus env polyprotein

  Query Match             61.0%;  Score 47;  DB 2;  Length 35;
  Best Local Similarity   64.3%;  Pred. No. 0.22;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 IQRGPGRAFVTIGK 15
          |  ||||||  | |:
Db     12 IHMGPGRAFYTTGE 25


RESULT 9
PC2295
V3 domain peptide P4317 - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 07-May-1999
C;Accession: PC2295
R;Sherefa, K.; Soennerborg, A.; Steinbergs, J.; Saellberg, M.
Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994
A;Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping a
A;Reference number: PC2291; MUID:95110306; PMID:7811250
A;Accession: PC2295
A;Molecule type: protein
A;Residues: 1-35 <SHE>
C;Superfamily: type E retrovirus env polyprotein

  Query Match             58.4%;  Score 45;  DB 2;  Length 35;
  Best Local Similarity   64.3%;  Pred. No. 0.49;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 IQRGPGRAFVTIGK 15
          |  ||||||  | |:
Db     12 IHIGPGRAFYTTGE 25


RESULT 10
S35809
envelope protein - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 26-Aug-1999
C;Accession: S35809
R;Chiodi, F.
submitted to the EMBL Data Library, June 1993
A;Reference number: S35800
A;Accession: S35809
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 <CHI>
A;Cross-references: EMBL:Z23187; NID:g313523; PIDN:CAA80708.1; PID:g313524
C;Superfamily: type E retrovirus env polyprotein

  Query Match             58.4%;  Score 45;  DB 2;  Length 77;
  Best Local Similarity   64.3%;  Pred. No. 1;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 IQRGPGRAFVTIGK 15
          |  ||||||  | |:
Db     37 IHIGPGRAFYTTGQ 50


RESULT 11
S35808
envelope protein - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 26-Aug-1999
C;Accession: S35808
R;Chiodi, F.
submitted to the EMBL Data Library, June 1993
A;Reference number: S35800
A;Accession: S35808
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 <CHI>
A;Cross-references: EMBL:Z23186; NID:g313521; PIDN:CAA80707.1; PID:g313522
C;Superfamily: type E retrovirus env polyprotein

  Query Match             58.4%;  Score 45;  DB 2;  Length 77;
  Best Local Similarity   64.3%;  Pred. No. 1;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 IQRGPGRAFVTIGK 15
          |  ||||||  | |:
Db     37 IHIGPGRAFYTTGQ 50


RESULT 12
S35848
envelope protein - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 26-Aug-1999
C;Accession: S35848
R;Chiodi, F.
submitted to the EMBL Data Library, June 1993
A;Reference number: S35800
A;Accession: S35848
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 <CHI>
A;Cross-references: EMBL:Z23232; NID:g313607; PIDN:CAA80750.1; PID:g313608
C;Superfamily: type E retrovirus env polyprotein

  Query Match             58.4%;  Score 45;  DB 2;  Length 77;
  Best Local Similarity   64.3%;  Pred. No. 1;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 IQRGPGRAFVTIGK 15
          |  ||||||  | |:
Db     37 IHIGPGRAFYTTGE 50


RESULT 13
S35815
envelope protein - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 26-Aug-1999
C;Accession: S35815
R;Chiodi, F.
```

submitted to the EMBL Data Library, June 1993
A;Reference number: S35800
A;Accession: S35815
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 <CHI>
A;Cross-references: EMBL:Z23193; NID:g313535; PIDN:CAA80714.1; PID:g313536
C;Superfamily: type E retrovirus env polyprotein

Query Match 58.4%; Score 45; DB 2; Length 77;
Best Local Similarity 64.3%; Pred. No. 1;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2 IQRGPGRAFVTIGK 15
           |  |||||| | |:
Db      37 IHIGPGRAFYTTGE 50
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RESULT 14
S35849
envelope protein - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 26-Aug-1999
C;Accession: S35849
R;Chiodi, F.
submitted to the EMBL Data Library, June 1993
A;Reference number: S35800
A;Accession: S35849
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 <CHI>
A;Cross-references: EMBL:Z23233; NID:g313609; PIDN:CAA80751.1; PID:g313610
C;Superfamily: type E retrovirus env polyprotein

Query Match 58.4%; Score 45; DB 2; Length 77;
Best Local Similarity 64.3%; Pred. No. 1;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy       2 IQRGPGRAFVTIGK 15
           |  |||||| | |:
Db      37 IHIGPGRAFYTTGE 50
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RESULT 15
S35861
envelope protein - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 26-Aug-1999
C;Accession: S35861
R;Chiodi, F.
submitted to the EMBL Data Library, June 1993
A;Reference number: S35800
A;Accession: S35861
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 <CHI>
A;Cross-references: EMBL:Z23245; NID:g313633; PIDN:CAA80763.1; PID:g313634
C;Superfamily: type E retrovirus env polyprotein

Query Match 58.4%; Score 45; DB 2; Length 77;
Best Local Similarity 64.3%; Pred. No. 1;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy       2 IQRGPGRAFVTIGK 15
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Db      37 INIGPGRAFYTTGE 50
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Search completed: March 10, 2003, 17:52:52
Job time : 21 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: March 10, 2003, 17:52:24 ; Search time 15 Seconds
(without alignments)
42.170 Million cell updates/sec

Title: US-09-191-772A-2
Perfect score: 77
Sequence: 1 RIQRGPGRAFVTIGK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	15	10	US-09-810-310-15	Sequence 15, Appl
2	77	100.0	15	10	US-09-810-310-24	Sequence 24, Appl
3	77	100.0	15	10	US-09-989-621-8	Sequence 8, Appli
4	77	100.0	20	10	US-09-813-659-3	Sequence 3, Appli
5	77	100.0	26	10	US-09-989-621-9	Sequence 9, Appli
6	77	100.0	30	10	US-09-810-310-6	Sequence 6, Appli
7	77	100.0	31	10	US-09-810-310-7	Sequence 7, Appli
8	77	100.0	35	10	US-09-810-310-1	Sequence 1, Appli
9	77	100.0	36	9	US-09-886-156-66	Sequence 66, Appl
10	77	100.0	36	9	US-09-886-150-66	Sequence 66, Appl
11	77	100.0	36	9	US-10-012-507-4	Sequence 4, Appli
12	77	100.0	36	9	US-09-886-149-66	Sequence 66, Appl
13	77	100.0	36	9	US-09-886-159-66	Sequence 66, Appl
14	77	100.0	39	10	US-09-810-310-2	Sequence 2, Appli
15	77	100.0	39	10	US-09-810-310-3	Sequence 3, Appli
16	77	100.0	42	10	US-09-810-310-5	Sequence 5, Appli
17	77	100.0	48	10	US-09-810-310-4	Sequence 4, Appli
18	77	100.0	511	10	US-09-796-202-17	Sequence 17, Appl
19	77	100.0	519	10	US-09-756-551A-8	Sequence 8, Appli
20	77	100.0	853	9	US-10-003-035-33	Sequence 33, Appl
21	77	100.0	856	10	US-09-476-242-1	Sequence 1, Appli
22	77	100.0	1101	9	US-10-003-035-53	Sequence 53, Appl
23	77	100.0	1186	9	US-10-003-035-55	Sequence 55, Appl
24	66	85.7	41	9	US-09-956-940-22	Sequence 22, Appl
25	66	85.7	41	9	US-09-956-940-25	Sequence 25, Appl
26	66	85.7	53	9	US-09-956-940-23	Sequence 23, Appl
27	62	80.5	20	9	US-09-827-345-24	Sequence 24, Appl
28	58	75.3	15	10	US-09-901-106-10	Sequence 10, Appl
29	57	74.0	17	10	US-09-901-106-12	Sequence 12, Appl
30	52	67.5	10	9	US-09-087-513-7	Sequence 7, Appli
31	52	67.5	10	9	US-09-087-513-13	Sequence 13, Appl
32	52	67.5	10	9	US-10-113-085-7	Sequence 7, Appli
33	52	67.5	10	9	US-09-997-848A-16	Sequence 16, Appl
34	52	67.5	10	10	US-09-858-349-3	Sequence 3, Appli
35	52	67.5	10	10	US-09-810-310-16	Sequence 16, Appl
36	52	67.5	10	10	US-09-820-484-8	Sequence 8, Appli
37	48	62.3	9	9	US-09-997-848A-1	Sequence 1, Appli
38	45	58.4	19	10	US-09-308-511-1	Sequence 1, Appli
39	45	58.4	376	9	US-09-934-060A-28	Sequence 28, Appl
40	45	58.4	502	10	US-09-796-202-16	Sequence 16, Appl
41	45	58.4	506	9	US-09-934-060A-24	Sequence 24, Appl
42	45	58.4	506	9	US-09-934-060A-30	Sequence 30, Appl
43	45	58.4	556	9	US-09-934-060A-6	Sequence 6, Appli
44	45	58.4	590	9	US-09-934-060A-13	Sequence 13, Appl
45	45	58.4	720	9	US-09-934-060A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-810-310-15
; Sequence 15, Application US/09810310
; Patent No. US20020044948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-15

Query Match 100.0%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
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Db 1 RIQRGPGRAFVTIGK 15

RESULT 2
US-09-810-310-24
; Sequence 24, Application US/09810310
; Patent No. US20020044948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF

; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-24

Query Match 100.0%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
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Db 1 RIQRGPGRAFVTIGK 15

RESULT 3
US-09-989-621-8
; Sequence 8, Application US/09989621
; Patent No. US20020151683A1
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Youn
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; TITLE OF INVENTION: Derived from X Protein of Hepatitis B virus
; FILE REFERENCE: 0136/0E154
; CURRENT APPLICATION NUMBER: US/09/989,621
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/051,006
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HIV
US-09-989-621-8

Query Match 100.0%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
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Db 1 RIQRGPGRAFVTIGK 15

RESULT 4
US-09-813-659-3
; Sequence 3, Application US/09813659
; Patent No. US20020012989A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; TITLE OF INVENTION: FUSION PROTEINS IN A MAMMALIAN CELL
; FILE REFERENCE: 30436.18USD2
; CURRENT APPLICATION NUMBER: US/09/813,659
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 09/549,067
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-659-3

Query Match 100.0%; Score 77; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
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Db 5 RIQRGPGRAFVTIGK 19

RESULT 5
US-09-989-621-9
; Sequence 9, Application US/09989621
; Patent No. US20020151683A1
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Youn
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; TITLE OF INVENTION: Derived from X Protein of Hepatitis B virus
; FILE REFERENCE: 0136/0E154
; CURRENT APPLICATION NUMBER: US/09/989,621
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/051,006
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 26
; TYPE: PRT
; ORGANISM: HIV
US-09-989-621-9

Query Match 100.0%; Score 77; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 12 RIQRGPGRAFVTIGK 26

RESULT 6
US-09-810-310-6
; Sequence 6, Application US/09810310
; Patent No. US20020044948A1

; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-6

Query Match 100.0%; Score 77; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
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Db 16 RIQRGPGRAFVTIGK 30

RESULT 7
US-09-810-310-7
; Sequence 7, Application US/09810310
; Patent No. US20020044948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-7

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Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
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Db 17 RIQRGPGRAFVTIGK 31

RESULT 8
US-09-810-310-1
; Sequence 1, Application US/09810310
; Patent No. US20020044948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-1

Query Match 100.0%; Score 77; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
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Db 21 RIQRGPGRAFVTIGK 35

RESULT 9
US-09-886-156-66
; Sequence 66, Application US/09886156
; Patent No. US20020155428A1
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495.0001-04
; CURRENT APPLICATION NUMBER: US/09/886,156
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US/09/109,916
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5
; PRIOR FILING DATE: 1992-10-06
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7
; PRIOR FILING DATE: 1992-10-22
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8
; PRIOR FILING DATE: 1992-12-30
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-886-156-66

Query Match 100.0%; Score 77; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
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Db 13 RIQRGPGRAFVTIGK 27

RESULT 10
US-09-886-150-66
; Sequence 66, Application US/09886150
; Patent No. US20020172939A1
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef

; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495.0001-04
; CURRENT APPLICATION NUMBER: US/09/886,150
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/109,916
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5
; PRIOR FILING DATE: 1992-10-06
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7
; PRIOR FILING DATE: 1992-10-22
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8
; PRIOR FILING DATE: 1992-12-30
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-886-150-66

Query Match 100.0%; Score 77; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
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Db 13 RIQRGPGRAFVTIGK 27

RESULT 11
US-10-012-507-4
; Sequence 4, Application US/10012507
; Patent No. US20020173446A1
; GENERAL INFORMATION:
; APPLICANT: Kwong, Peter
; APPLICANT: Hendrickson, Wayne
; APPLICANT: Wyatt, Richard
; APPLICANT: Sodroski, Joseph
; TITLE OF INVENTION: COMPOUNDS WHICH BIND TO THE CENTRAL CAVITY BETWEEN HIV-1 gp120 AN
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 0575/63618-A
; CURRENT APPLICATION NUMBER: US/10/012,507
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: HXBc2 (a laboratory - adapted HIV-1 isolate)
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(36)
; OTHER INFORMATION: V3 loop of gp120 core
US-10-012-507-4

Query Match 100.0%; Score 77; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
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Db 13 RIQRGPGRAFVTIGK 27

RESULT 12
US-09-886-149-66
; Sequence 66, Application US/09886149
; Publication No. US20030003442A1
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495.0001-04
; CURRENT APPLICATION NUMBER: US/09/886,149
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/109,916
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5
; PRIOR FILING DATE: 1992-10-06
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7
; PRIOR FILING DATE: 1992-10-22
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8
; PRIOR FILING DATE: 1992-12-30
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-886-149-66

Query Match 100.0%; Score 77; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
||||||||||||||||
Db 13 RIQRGPGRAFVTIGK 27

RESULT 13
US-09-886-159-66
; Sequence 66, Application US/09886159
; Publication No. US20030003443A1
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495.0001-04
; CURRENT APPLICATION NUMBER: US/09/886,159
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US/09/109,916
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5
; PRIOR FILING DATE: 1992-10-06
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7
; PRIOR FILING DATE: 1992-10-22
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8
; PRIOR FILING DATE: 1992-12-30
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-886-159-66

Query Match 100.0%; Score 77; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RIQRGPGRAFVTIGK 15
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Db     13 RIQRGPGRAFVTIGK 27


RESULT 14
US-09-810-310-2
; Sequence 2, Application US/09810310
; Patent No. US20020044948A1
; GENERAL INFORMATION:
;  APPLICANT: Khleif, Samir N.
;  APPLICANT:  Berzofsky, Jay A.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
;  TITLE OF INVENTION:  IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
;  FILE REFERENCE: 15280-415100US
;  CURRENT APPLICATION NUMBER: US/09/810,310
;  CURRENT FILING DATE:  2001-03-14
;  PRIOR APPLICATION NUMBER: 60/189,396
;  PRIOR FILING DATE: 2000-03-15
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
;   OTHER INFORMATION: ANTIGEN
US-09-810-310-2

  Query Match             100.0%;  Score 77;  DB 10;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
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Db     25 RIQRGPGRAFVTIGK 39


RESULT 15
US-09-810-310-3
; Sequence 3, Application US/09810310
; Patent No. US20020044948A1
; GENERAL INFORMATION:
;  APPLICANT: Khleif, Samir N.
;  APPLICANT:  Berzofsky, Jay A.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
;  TITLE OF INVENTION:  IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
;  FILE REFERENCE: 15280-415100US
;  CURRENT APPLICATION NUMBER: US/09/810,310
;  CURRENT FILING DATE:  2001-03-14
;  PRIOR APPLICATION NUMBER: 60/189,396
;  PRIOR FILING DATE: 2000-03-15
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 39
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
;   OTHER INFORMATION: ANTIGEN
US-09-810-310-3

  Query Match             100.0%;  Score 77;  DB 10;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db     25 RIQRGPGRAFVTIGK 39


Search completed: March 10, 2003, 18:02:04
Job time : 16 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: March 10, 2003, 17:50:39 ; Search time 16 Seconds
(without alignments)
27.584 Million cell updates/sec

Title: US-09-191-772A-2
Perfect score: 77
Sequence: 1 RIQRGPGRAFVTIGK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	100.0	15	1	US-08-336-087-2	Sequence 2, Appli
2	77	100.0	15	1	US-08-218-025A-17	Sequence 17, Appl
3	77	100.0	15	1	US-08-709-047-7	Sequence 7, Appli
4	77	100.0	15	1	US-08-479-400-2	Sequence 2, Appli
5	77	100.0	15	1	US-08-410-360-7	Sequence 7, Appli
6	77	100.0	15	1	US-08-095-332-1	Sequence 1, Appli
7	77	100.0	15	1	US-08-707-801A-7	Sequence 7, Appli
8	77	100.0	15	1	US-08-709-006-7	Sequence 7, Appli
9	77	100.0	15	1	US-08-711-175-7	Sequence 7, Appli
10	77	100.0	15	1	US-08-488-252-27	Sequence 27, Appl
11	77	100.0	15	2	US-08-021-879-2	Sequence 2, Appli
12	77	100.0	15	2	US-07-760-530-1	Sequence 1, Appli
13	77	100.0	15	2	US-07-950-571A-3	Sequence 3, Appli
14	77	100.0	15	2	US-08-975-699-6	Sequence 6, Appli
15	77	100.0	15	2	US-08-972-089-6	Sequence 6, Appli
16	77	100.0	15	2	US-08-455-625-7	Sequence 7, Appli
17	77	100.0	15	2	US-08-395-204-2	Sequence 2, Appli
18	77	100.0	15	2	US-08-628-687-1	Sequence 1, Appli
19	77	100.0	15	2	US-07-847-311A-1	Sequence 1, Appli
20	77	100.0	15	2	US-08-986-234-13	Sequence 13, Appl
21	77	100.0	15	2	US-08-986-234-28	Sequence 28, Appl
22	77	100.0	15	3	US-08-492-076-22	Sequence 22, Appl
23	77	100.0	15	3	US-08-493-071-25	Sequence 25, Appl
24	77	100.0	15	4	US-08-480-332-1	Sequence 1, Appli
25	77	100.0	15	4	US-08-455-685-7	Sequence 7, Appli
26	77	100.0	15	4	US-08-060-988A-7	Sequence 7, Appli
27	77	100.0	15	4	US-09-051-006-8	Sequence 8, Appli
28	77	100.0	15	5	PCT-US92-10378-1	Sequence 1, Appli
29	77	100.0	15	5	PCT-US94-05142-7	Sequence 7, Appli
30	77	100.0	16	2	US-08-657-392-28	Sequence 28, Appl
31	77	100.0	16	2	US-08-251-472-2	Sequence 2, Appli
32	77	100.0	16	2	US-08-484-905-35	Sequence 35, Appl
33	77	100.0	16	3	US-08-481-985B-35	Sequence 35, Appl
34	77	100.0	16	3	US-09-248-082-2	Sequence 2, Appli
35	77	100.0	16	4	US-08-370-476-35	Sequence 35, Appl
36	77	100.0	16	4	US-08-992-877-15	Sequence 15, Appl
37	77	100.0	16	5	PCT-US94-02539-28	Sequence 28, Appl
38	77	100.0	18	1	US-08-015-770B-4	Sequence 4, Appli
39	77	100.0	20	1	US-08-121-054C-3	Sequence 3, Appli
40	77	100.0	20	1	US-08-488-252-28	Sequence 28, Appl
41	77	100.0	20	4	US-08-539-436-3	Sequence 3, Appli
42	77	100.0	21	2	US-08-452-503A-4	Sequence 4, Appli
43	77	100.0	21	2	US-08-453-745A-4	Sequence 4, Appli
44	77	100.0	21	2	US-08-470-419-25	Sequence 25, Appl
45	77	100.0	21	2	US-08-648-298-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-336-087-2
; Sequence 2, Application US/08336087
; Patent No. 5503829
; GENERAL INFORMATION:
; APPLICANT: Ladant, Daniel
; APPLICANT: Leclerc, Claude
; APPLICANT: Sebo, Peter
; APPLICANT: Ullmann, Agnes
; TITLE OF INVENTION: Recombinant Mutants for Inducing
; TITLE OF INVENTION: Specific Immune Responses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,087
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/011,644
; FILING DATE: 29-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495-0109-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-336-087-2

Query Match 100.0%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RIQRGPGRAFVTIGK 15
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Db      1 RIQRGPGRAFVTIGK 15


RESULT 2
US-08-218-025A-17
; Sequence 17, Application US/08218025A
; Patent No. 5556744
;  GENERAL INFORMATION:
;    APPLICANT:  Weiner, David B.
;    APPLICANT:  Ugen, Kenneth E.
;    APPLICANT:  Williams, William V.
;    TITLE OF INVENTION:  Methods and Compositions for Diagnosing
;    TITLE OF INVENTION:  and Treating Certain HIV Infected Patients
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  P.O. Box 457, 321 No. 5556744ristown Road
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/218,025A
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/891,451
;      FILING DATE:  29-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST33A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 540-9206
;      TELEFAX:  (215) 540-5818
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-218-025A-17

 Query Match             100.0%;  Score 77;  DB 1;  Length 15;
 Best Local Similarity   100.0%;  Pred. No. 3.7e-06;
 Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db      1 RIQRGPGRAFVTIGK 15


RESULT 3
US-08-709-047-7
; Sequence 7, Application US/08709047
; Patent No. 5652333
;  GENERAL INFORMATION:
;    APPLICANT:  Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y., Kim, Young W., Yu,
;    APPLICANT:  Liming
;    TITLE OF INVENTION:  THE gC1q RECEPTOR, HIV-1 gp120 REGION BINDING THERETO,
;    TITLE OF INVENTION:  AND RELATED PEPTIDES AND TARGETING ANTIBODIES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Tanox Biosystems, Inc.
;      STREET:  10301 Stella Link Rd.
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  DOS 3.30
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,047
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/410,360
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mirabel, Eric P.
;      REGISTRATION NUMBER:  31,211
;      REFERENCE/DOCKET NUMBER:  TNX95-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 664-2288
;      TELEFAX:  (713) 664-8914
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-709-047-7

 Query Match             100.0%;  Score 77;  DB 1;  Length 15;
 Best Local Similarity   100.0%;  Pred. No. 3.7e-06;
 Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db      1 RIQRGPGRAFVTIGK 15


RESULT 4
US-08-479-400-2
; Sequence 2, Application US/08479400
; Patent No. 5679784
;  GENERAL INFORMATION:
;    APPLICANT:  Ladant, Daniel
;    APPLICANT:  Leclerc, Claude
;    APPLICANT:  Sebo, Peter
;    APPLICANT:  Ullmann, Agnes
;    TITLE OF INVENTION:  Recombinant Mutants for Inducing
;    TITLE OF INVENTION:  Specific Immune Responses
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/479,400
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/011,644
;      FILING DATE:  29-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
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;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  03495-0109-01000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-479-400-2

  Query Match           100.0%;  Score 77;  DB 1;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
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Db      1 RIQRGPGRAFVTIGK 15


RESULT 5
US-08-410-360-7
; Sequence 7, Application US/08410360
; Patent No. 5691447
;  GENERAL INFORMATION:
;    APPLICANT:  Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y., Kim, Young W., Yu,
;    APPLICANT:  Liming
;    TITLE OF INVENTION:  THE gC1q RECEPTOR, HIV-1 gp120 REGION BINDING THERETO,
;    TITLE OF INVENTION:  AND RELATED PEPTIDES AND TARGETING ANTIBODIES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Tanox Biosystems, Inc.
;      STREET:  10301 Stella Link Rd.
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  DOS 3.30
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/410,360
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mirabel, Eric P.
;      REGISTRATION NUMBER:  31,211
;      REFERENCE/DOCKET NUMBER:  TNX95-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 664-2288
;      TELEFAX:  (713) 664-8914
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-410-360-7

  Query Match           100.0%;  Score 77;  DB 1;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
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Db      1 RIQRGPGRAFVTIGK 15


RESULT 6
US-08-095-332-1
; Sequence 1, Application US/08095332
; Patent No. 5711947
;  GENERAL INFORMATION:
;    APPLICANT:  Berzofsky, Jay A.
;    APPLICANT:  Takahashi, Hidemi
;    APPLICANT:  Germain, Ronald N.
;    TITLE OF INVENTION:  METHOD TO INDUCE CYTOTOXIC T LYMPHOCYTES
;    TITLE OF INVENTION:  SPECIFIC FOR A BROAD ARRAY OF HIV-1 ISOLATES USING HYBRID
;    TITLE OF INVENTION:  SYNTHETIC PEPTIDES
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Birch, Stewart, Kolash & Birch
;      STREET:  301 N. Washington
;      CITY:  Falls Church
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22046-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/095,332
;      FILING DATE:  23-JUL-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/760,530
;      FILING DATE:  18-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svensson, Leonard R.
;      REGISTRATION NUMBER:  30,330
;      REFERENCE/DOCKET NUMBER:  1173-354p
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-241-1300
;      TELEFAX:  703-241-2848
;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  HIV-1
;      INDIVIDUAL ISOLATE:  IIIB
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..15
;      OTHER INFORMATION:  /label= peptide
;      OTHER INFORMATION:  /note= "synthetic peptide, sequence = residues 315
;      OTHER INFORMATION:  to 329 of HIV-1, isolate IIIB, gp160 envelope
;      OTHER INFORMATION:  glycoprotein."
US-08-095-332-1

  Query Match           100.0%;  Score 77;  DB 1;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db      1 RIQRGPGRAFVTIGK 15


RESULT 7
US-08-707-801A-7
; Sequence 7, Application US/08707801A
; Patent No. 5728814
;  GENERAL INFORMATION:
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```
;    APPLICANT:  Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y., Kim, Young W., Yu,
;    APPLICANT:  Liming
;    TITLE OF INVENTION:  THE gC1q RECEPTOR, HIV-1 gp120 REGION BINDING THERETO,
;    TITLE OF INVENTION:  AND RELATED PEPTIDES AND TARGETING ANTIBODIES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Tanox Biosystems, Inc.
;      STREET:  10301 Stella Link Rd.
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  DOS 3.30
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/707,801A
;      FILING DATE:  09/04/1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/410,360
;      FILING DATE:  03/24/1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mirabel, Eric P.
;      REGISTRATION NUMBER:  31,211
;      REFERENCE/DOCKET NUMBER:  TNX95-1AA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 664-2288
;      TELEFAX:  (713) 664-8914
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-707-801A-7

  Query Match             100.0%;  Score 77;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db       1 RIQRGPGRAFVTIGK 15


RESULT 8
US-08-709-006-7
; Sequence 7, Application US/08709006
; Patent No. 5731428
;  GENERAL INFORMATION:
;    APPLICANT:  Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y.,
;    APPLICANT:  Kim, Young W., Yu, Liming
;    TITLE OF INVENTION:  THE gC1q RECEPTOR, HIV-1 gp120 REGION BINDING
;    TITLE OF INVENTION:  THERETO, AND RELATED PEPTIDES AND TARGETING
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Tanox Biosystems, Inc.
;      STREET:  10301 Stella Link Rd.
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  DOS 3.30
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,006
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/410,360
;      FILING DATE:  24-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mirabel, Eric P.
;      REGISTRATION NUMBER:  31,211
;      REFERENCE/DOCKET NUMBER:  TNX95-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 664-2288
;      TELEFAX:  (713) 664-8914
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-709-006-7

  Query Match             100.0%;  Score 77;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
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Db       1 RIQRGPGRAFVTIGK 15


RESULT 9
US-08-711-175-7
; Sequence 7, Application US/08711175
; Patent No. 5739306
;  GENERAL INFORMATION:
;    APPLICANT:  Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y.,
;    APPLICANT:  Kim, Young W., Yu, Liming
;    TITLE OF INVENTION:  THE gC1q RECEPTOR, HIV-1 gp120 REGION BINDING
;    TITLE OF INVENTION:  THERETO, AND RELATED PEPTIDES AND TARGETING
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Tanox Biosystems, Inc.
;      STREET:  10301 Stella Link Rd.
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  DOS 3.30
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/711,175
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/410,360
;      FILING DATE:  24-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mirabel, Eric P.
;      REGISTRATION NUMBER:  31,211
;      REFERENCE/DOCKET NUMBER:  TNX95-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 664-2288
;      TELEFAX:  (713) 664-8914
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-711-175-7

  Query Match             100.0%;  Score 77;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-06;
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db      1 RIQRGPGRAFVTIGK 15


RESULT 10
US-08-488-252-27
; Sequence 27, Application US/08488252
; Patent No. 5763160
;  GENERAL INFORMATION:
;    APPLICANT:  Chang Yi Wang
;    TITLE OF INVENTION:  SYNTHETIC PEPTIDES AND PROCESS
;    TITLE OF INVENTION:  OF USING SAME FOR THE DETECTION OF ANTIBODIES TO
;    TITLE OF INVENTION:  HUMAN IMMUNODEFICIENCY VIRUS (HIV) GP120 ENVELOPE
;    TITLE OF INVENTION:  PROTEIN, DIAGNOSIS OF AIDS AND PRE-AIDS CONDITIONS
;    TITLE OF INVENTION:  AND AS VACCINES
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVE.
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,252
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08\326,676
;      FILING DATE:  07-Jun-1995
;      APPLICATION NUMBER:  07\726,605
;      FILING DATE:  09-July-1991
;      APPLICATION NUMBER:  07\663,262
;      FILING DATE:  01-Mar-1991
;      APPLICATION NUMBER:  07\155,321
;      FILING DATE:  12-Feb-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria C. H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4004 US4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  (212) 751-6849
;      TELEX:  421792
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  Amino acids
;      STRANDEDNESS:
;      TOPOLOGY:  Unknown
US-08-488-252-27

  Query Match             100.0%;  Score 77;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
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Db      1 RIQRGPGRAFVTIGK 15


RESULT 11
US-08-021-879-2
; Sequence 2, Application US/08021879
; Patent No. 5817767
;  GENERAL INFORMATION:
;    APPLICANT:  Graham P. Allaway
;    APPLICANT:  Paul J. Maddon
;    TITLE OF INVENTION:  SYNERGISTIC COMPOSITION OF CD4-BASED
;    TITLE OF INVENTION:  PROTEIN AND ANTI-HIV-1 ANTIBODY, AND
;    TITLE OF INVENTION:  METHODS OF USING SAME
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/021,879
;      FILING DATE:  24-FEB-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  41189/JPW/AJM
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 977-9550
;      TELEFAX:  (212) 664-0525
;      TELEX:  422523 COOPUI
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-021-879-2

  Query Match             100.0%;  Score 77;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db      1 RIQRGPGRAFVTIGK 15


RESULT 12
US-07-760-530-1
; Sequence 1, Application US/07760530
; Patent No. 5820865
;  GENERAL INFORMATION:
;    APPLICANT:  Berzofsky, Jay A.
;    APPLICANT:  Takahashi, Hidemi
;    APPLICANT:  Germain, Ronald N.
;    TITLE OF INVENTION:  METHOD TO INDUCE CYTOTOXIC T LYMPHOCYTES
;    TITLE OF INVENTION:  SPECIFIC FOR A BROAD ARRAY OF HIV-1 ISOLATES USING HYBRID
;    TITLE OF INVENTION:  SYNTHETIC PEPTIDES
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Birch, Stewart, Kolash & Birch
;      STREET:  301 N. Washington
;      CITY:  Falls Church
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22046-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/07/760,530
;       FILING DATE:  19910918
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Svensson, Leonard R.
;       REGISTRATION NUMBER:  30,330
;       REFERENCE/DOCKET NUMBER:  1173-354p
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  703-241-1300
;       TELEFAX:  703-241-2848
;       TELEX:  248345
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
;       ORGANISM:  HIV-1
;       INDIVIDUAL ISOLATE:  IIIB
;     FEATURE:
;       NAME/KEY:  Peptide
;       LOCATION:  1..15
;       OTHER INFORMATION:  /label= peptide
;       OTHER INFORMATION:  /note= "synthetic peptide, sequence = residues 315
;       OTHER INFORMATION:  to 329 of HIV-1, isolate IIIB, gp160 envelope
;       OTHER INFORMATION:  glycoprotein."
US-07-760-530-1

  Query Match             100.0%;  Score 77;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           |||||||||||||||
Db       1 RIQRGPGRAFVTIGK 15


RESULT 13
US-07-950-571A-3
; Sequence 3, Application US/07950571A
; Patent No. 5854400
;  GENERAL INFORMATION:
;    APPLICANT:  Chang, Tse Wen,  Fung, Michael S.C.,  Sun, Bill N.C.,  Sun, Cecily R.Y.
;    APPLICANT:  Chang, Nancy T.
;    TITLE OF INVENTION:  Monoclonal Antibodies which Neutralize HIV-1 Infection
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Tanox Biosystems, Inc.
;      STREET:  10301 Stella Link Rd.
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Hi Density Diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  DOS, Version 3.30
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/950,571A
;      FILING DATE:  19920922
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  No. 5854400 07/767,533
;      FILING DATE:  09/26/1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mirabel, Eric P.
;      REGISTRATION NUMBER:  31,211
;      REFERENCE/DOCKET NUMBER:  TNX87-11BBC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713-664-2288
;      TELEFAX:  713-664-8914
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  Linear
US-07-950-571A-3

  Query Match             100.0%;  Score 77;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
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Db       1 RIQRGPGRAFVTIGK 15


RESULT 14
US-08-975-699-6
; Sequence 6, Application US/08975699
; Patent No. 5858369
;  GENERAL INFORMATION:
;    APPLICANT:  MATSUO, KAZUHIRO
;    APPLICANT:  CHUJO, YOSHITOMO
;    APPLICANT:  YAMAZAKI, AKIHIRO
;    APPLICANT:  HONDA, MITSUO
;    APPLICANT:  YAMAKAZI, SHUDO
;    APPLICANT:  TASAKA, HIROMICHI
;    TITLE OF INVENTION:  ANTI-AIDS SECRETORY RECOMBINANT BCG
;    TITLE OF INVENTION:  VACCINE
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON. SPIVAK, MCCCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/975,699
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/619,512
;      FILING DATE:  29-MAR-1996
;      APPLICATION NUMBER:  PCT/JP95/01515
;      FILING DATE:  31-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 178462/1994
;      FILING DATE:  29-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  10-795-0X PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  HUMAN IMMUNODEFICIENCY VIRUS
;      STRAIN:  HIV-1 (JAPAN)
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US-08-975-699-6

Query Match 100.0%; Score 77; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
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Db 1 RIQRGPGRAFVTIGK 15

RESULT 15
US-08-972-089-6
; Sequence 6, Application US/08972089
; Patent No. 5885580
; GENERAL INFORMATION:
; APPLICANT: MATSUO, KAZUHIRO
; APPLICANT: CHUJO, YOSHITOMO
; APPLICANT: YAMAZAKI, AKIHIRO
; APPLICANT: HONDA, MITSUO
; APPLICANT: YAMAKAZI, SHUDO
; APPLICANT: TASAKA, HIROMICHI
; TITLE OF INVENTION: ANTI-AIDS SECRETORY RECOMBINANT BCG
; TITLE OF INVENTION: VACCINE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON. SPIVAK, MCCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,089
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,699
; FILING DATE:
; APPLICATION NUMBER: PCT/JP95/01515
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 178462/1994
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-795-0X PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; STRAIN: HIV-1 (JAPAN)
US-08-972-089-6

Query Match 100.0%; Score 77; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RIQRGPGRAFVTIGK 15

Search completed: March 10, 2003, 17:58:27
Job time : 17 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: March 10, 2003, 17:41:23 ; Search time 36 Seconds
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Title: US-09-191-772A-2
Perfect score: 77
Sequence: 1 RIQRGPGRAFVTIGK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	77	100.0	15	10	AAP91228	Peptide comprising
3	77	100.0	15	13	AAR21343	Sequence of antige
4	77	100.0	15	14	AAR32207	Sequence of peptid
5	77	100.0	15	14	AAR38187	V3 loop peptide D4
6	77	100.0	15	15	AAR51619	V3 loop region of
7	77	100.0	15	16	AAR74603	HIV-I variable loo
8	77	100.0	15	16	AAR68789	Cytotoxic T lympho
9	77	100.0	15	16	AAR66414	HIV-1 IIIB peptide
10	77	100.0	15	17	AAW07931	gp120 peptide p18p
11	77	100.0	15	17	AAW05535	HIV-1 gp120 peptid
12	77	100.0	15	17	AAR92007	HIV-1 V3 loop epit
13	77	100.0	15	17	AAR92033	Hydrophilic peptid
14	77	100.0	15	18	AAW24219	CD4+ T-lymphocyte
15	77	100.0	15	18	AAW22031	Antigenic human im
16	77	100.0	15	18	AAW10348	HIV epitope env P1
17	77	100.0	15	19	AAW76898	Fusion immunoglobu
18	77	100.0	15	19	AAW54929	HIV gp120 envelope
19	77	100.0	15	19	AAW40316	HIV-1 IIIB gp120 p
20	77	100.0	15	19	AAW39275	HIV-1 synthetic pe
21	77	100.0	15	20	AAY24466	HIV peptide R15K-1
22	77	100.0	15	20	AAY25189	HIV protein gp160
23	77	100.0	15	20	AAY25204	HIV V3 peptide fra
24	77	100.0	15	20	AAY05356	HIV-1 CLUVAC pepti
25	77	100.0	15	20	AAY06896	Sequence of gp120I
26	77	100.0	15	20	AAY04680	HIV-1 gp120 amino
27	77	100.0	15	20	AAW87620	Epitope of HIV-1 g
28	77	100.0	15	20	AAW72821	HIV-1 gp120 monocl
29	77	100.0	15	21	AAY85591	HIV related peptid
30	77	100.0	15	21	AAB15875	Human chemokine de
31	77	100.0	15	21	AAY83916	HIV-1 env T-cell e
32	77	100.0	15	21	AAY66439	HLA-A2-binding HIV
33	77	100.0	15	21	AAY66455	HLA-A3-binding HIV
34	77	100.0	15	22	AAB92345	Virus related pept
35	77	100.0	15	22	AAB92348	Virus related pept
36	77	100.0	15	22	AAB68601	HIV gp120 V3 loop
37	77	100.0	15	23	ABG68654	HIV-1 P18IIIB pept
38	77	100.0	15	23	ABG68663	HIV-1 P18 based pe
39	77	100.0	15	23	AAU97690	HIV CTL epitope pe
40	77	100.0	15	23	AAU96031	HIV epitope, HIV-1
41	77	100.0	15	23	AAE15743	Human immunodefici
42	77	100.0	16	13	AAR24939	HIV peptide ENV 31
43	77	100.0	16	19	AAW68326	MHC binding peptid
44	77	100.0	16	21	AAY68203	Altered MHC determ
45	77	100.0	16	21	AAY52857	Altered MHC determ

ALIGNMENTS

RESULT 1
AAP82095
ID AAP82095 standard; peptide; 15 AA.
XX
AC AAP82095;
XX
DT 17-DEC-2001 (updated)
DT 29-OCT-1990 (first entry)
XX
DE Env-K1 peptide.
XX
KW Env-K1; gp160 Env protein; T-cell cytotoxicity; HIV.
XX
OS synthetic.
XX
PN USN7148692-N.
XX
PD 02-AUG-1988.
XX
PF 26-JAN-1988; 88US-0192059.
XX
PR 26-JAN-1988; 88US-0148692.
XX
PA (USSH) US DEPT HEALTH AND HUMAN.
PA (USDC) US SEC OF COMMERCE.
XX
PI Berzofsky J, Takahashi H, Hosmalin A, Germain R, Moss B;
XX
DR WPI; 1988-264280/37.
XX
PT Synthetic peptide corresp. to HIV gp 160 Env sequence -
PT which elicits cytotoxicity by T cells against HIV and
PT proliferation of HIV-specific T cells

```
XX
PS   Disclosure; ; pp; English.
XX
CC   This peptide elicits cytotoxicity by T-cells against HIV antigens
CC   and stimulates prodn. of HIV-specific cytotoxic T-lymphocytes
CC   (CTLs).  It is specific for the HIV envelope protein gp160.
CC   (Note: Revised entry submitted to correct the patent number format of
CC   US Government-owned NTIS applications to prevent clashes with ongoing US
CC   granted patent numbers. For further information please visit the Derwent
CC   web site at www.derwent.com/dwpi/updates/ntis_us.html.)
XX
SQ   Sequence   15 AA;

  Query Match             100.0%;  Score 77;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db      1 RIQRGPGRAFVTIGK 15


RESULT 2
AAP91228
ID   AAP91228 standard; peptide; 15 AA.
XX
AC   AAP91228;
XX
DT   13-AUG-1990  (first entry)
XX
DE   Peptide comprising AAs 308-322 of HIV-I IIIB env protein.
XX
KW   AIDS; HIV-I; vaccine.
XX
OS   HIV-I.
XX
PN   EP339504-A.
XX
PD   02-NOV-1989.
XX
PF   21-APR-1989;   89EP-0107197.
XX
PR   20-MAR-1989;   89US-0324027.
PR   26-APR-1988;   88US-0186333.
XX
PA   (DUPO ) DUPONT DE NEMOURS CO.
XX
PI   Kenealy WR,  Petteway SR,  Durda PJ;
XX
DR   WPI; 1989-317386/44.
XX
PT   Synthetic human immuno-deficiency virus env-coded peptide(s) -
PT   induce antibodies that block human immuno-deficiency virus
PT   proliferation and fusion between infected and non-infected cells.
XX
PS   Claim 3; Page 21; 24pp; English.
XX
CC   Peptide will induce an immune response in subject, and will thus act as a
CC   non-infective vaccine, prophylactic or have therapuetic value for AIDS
CC   patients.
XX
SQ   Sequence   15 AA;

  Query Match             100.0%;  Score 77;  DB 10;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db      1 RIQRGPGRAFVTIGK 15


RESULT 3
AAR21343
ID   AAR21343 standard; Protein; 15 AA.
XX
AC   AAR21343;
XX
DT   16-MAY-1992  (first entry)
XX
DE   Sequence of antigenic determinant (epitope) within gp120 that is
DE   recognised by mouse immunoglobulin BAT123 and mouse/human chimeric
DE   antibody CAG1-51-4.
XX
KW   Chimeric immunoglobulin; viral-neutralising; HIV-1;
KW   BAT123 mouse immunoglobulin; viral antigen-binding region;
KW   immunotherapy; AIDS; ARC; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   WO9201719-A.
XX
PD   06-FEB-1992.
XX
PF   18-JUL-1990;   90WO-US04048.
XX
PR   18-JUL-1990;   90WO-US04048.
XX
PA   (TANO-) TANOX BIOSYST INC.
XX
PI   Liov RS,  Rosen EM,  Sun BN,  Fung MS,  Chang TW,  Chang NT;
XX
DR   WPI; 1992-064897/08.
XX
PT   New chimeric HIV-1-neutralising immunoglobulin(s) - comprising
PT   non-human antigen binding regions and constant human region, for
PT   immuno-therapy of AIDS and ARC
XX
PS   Example; Page 26; 39pp; English.
XX
CC   The inventors claim a chimeric, viral-neutralising immunoglobulin
CC   which binds to the gp120 region of HIV-1 with a potency and
CC   immunologic specificity equal to BAT123 mouse Ig. It comprises a
CC   viral-specific antigen-binding region of non-human origian and a
CC   constant region of human origin. Specifically claimed is the chimeric
CC   immunoglobulin CGP 47439. Probes V-kappa-1 and V-kappa-2 (AAQ21497,
CC   AAQ21498) were used to screen a genomic DNA library for BAT123 cells
CC   for the functionally rearranged variable region gene of BAT123 light
CC   chaim (VL). The identified clone, V-kappa-123-23, was used in the
CC   subsequent construction of the mouse/human chimeric L chain gene.
CC   Probe VH-1 was used to screen partial genomic libraries for the
CC   functionally rearranged variable region genes for BAT123 heavy
CC   chain (VH). Clone VH-123-E3 hybridised with the probe. This clone
CC   was used in the construction of the mouse-human chimeric H chain
CC   gene.The chimeric antibody CAG1-51-4 was found to bind to the same
CC   oligopeptide (AAR21343) as BAT123 which indicates that the
CC   antigen specificity of the murine antibody BAT123 was preserved
CC   upon conversion into a mouse/human chimeric antibody.
XX
SQ   Sequence   15 AA;

  Query Match             100.0%;  Score 77;  DB 13;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db      1 RIQRGPGRAFVTIGK 15


RESULT 4
AAR32207
ID   AAR32207 standard; peptide; 15 AA.
XX
AC   AAR32207;
XX
```

DT 17-DEC-2001 (updated)
DT 07-JUN-1993 (first entry)
XX
DE Sequence of peptide which corresp.to AA residues 315-329 of the V3
DE loop of the gp160 envelope glycoprotein in HIV-1 strain MN.
XX
KW V3 loop; envelope glycoprotein; gp160; HIV-1; prophylaxis;
KW immunotherapy.
XX
OS Human immunodeficiency virus (HIV-1) isolate IIIB.
XX
PN USN7760530-N.
XX
PD 15-DEC-1992.
XX
PF 18-SEP-1991; 91US-0760530.
XX
PR 18-SEP-1991; 91US-0760530.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
XX
PI Berzofsky JA, Germain RN, Takahashi H;
XX
DR WPI; 1993-058406/07.
XX
PT Peptide(s) corresponding to the V3 loop of gp=160 of HIV-1 -
PT elicit cytotoxic T lymphocyte(s) active against broad range of
PT HIV-1 isolate(s)
XX
PS Example; Page 19; 41pp; English.
XX
CC The peptide corresponds to amino acid residues numbered 315-329 in
CC the V3 loop of the envelope glycoprotein gp160 of human
CC immunodeficiency virus (HIV-1), as numbered by Ratner in the strain
CC MN. It is useful for the prophylaxis or immunotherapy of HIV-1
CC infection. It elicits an immunised subject ctytoxic T lymphocyte
CC (CTL) activity against the corresp. clinical isolate of HIV-1.
CC (Note: Revised entry submitted to correct the patent number format of
CC US Government-owned NTIS applications to prevent clashes with ongoing US
CC granted patent numbers. For further information please visit the Derwent
CC web site at www.derwent.com/dwpi/updates/ntis_us.html.)
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
||||||||||||||||
Db 1 RIQRGPGRAFVTIGK 15

RESULT 5
AAR38187
ID AAR38187 standard; peptide; 15 AA.
XX
AC AAR38187;
XX
DT 12-OCT-1993 (first entry)
XX
DE V3 loop peptide D44 (R15K).
XX
KW gp120; HIV-1; cytotoxic T-lymphocyte; CTL; T-helper;
KW AIDS; infection.
XX
OS Human immunodeficiency virus-1 strain IIIB.
XX
PN WO9310816-A.
XX
PD 10-JUN-1993.
XX
PF 02-DEC-1992; 92WO-US10378.
XX
PR 02-DEC-1991; 91US-0800932.
PR 16-SEP-1992; 92US-0945865.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Arlinghaus RB, Nehete PN, Platsoucas CD, Sastry JK;
XX
DR WPI; 1993-196739/24.
XX
PT Peptide composition for treating and preventing viral infections
PT - comprise CTL-inducing epitope and HIV infection-inhibiting
PT sequence or T helper cell-inducing sequence
XX
PS Claim 13 + 19; Page 94-95; 130pp; English.
XX
CC HIV gp120 V3 loop-derived peptides (AAR38170-87) are successful in
CC generating CTL responses, esp. peptide R15K (AAR38187); the T-helper
CC cell-inducing peptide includes the sequence C19A (AAR38164);
CC HIV infection-inhibiting peptides are given in AAR38188-206, and are
CC esp. peptides R15K, N24G, E13V, R8K, T13Q and H13N (AAR38165-69).
CC The peptides may also be derived from an influenza virus protein or
CC a sendai virus protein (AAR41014-15).
CC It was observed that peptide R15K (amino acids 315-329), with sequences
CC derived from the V3 loop of HIV-1 IIIB, inhibits HIV-1 infection of
CC primary human T cells by 92% at 1 microg/ml (ca. 0.4-0.6 microM).
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
||||||||||||||||
Db 1 RIQRGPGRAFVTIGK 15

RESULT 6
AAR51619
ID AAR51619 standard; Protein; 15 AA.
XX
AC AAR51619;
XX
DT 21-OCT-1994 (first entry)
XX
DE V3 loop region of gp120 of HIV.
XX
KW gp 120; HIV epitope;
KW Human Immunodeficiency Virus fusion polypeptide.
XX
OS Human Immunodeficiency Virus.
XX
PN WO9406469-A.
XX
PD 31-MAR-1994.
XX
PF 18-SEP-1992; 92WO-US07966.
XX
PR 18-SEP-1992; 92WO-US07966.
XX
PA (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.
XX
PI Altman A, Baier GJ;
XX
DR WPI; 1994-118166/14.
XX
PT New fusion polypeptide of antigen binding domain and HIV epitope
PT - useful as vaccine for treatment or prevention of HIV infection,
PT ensures efficient focusing of epitopes on surface of antigen
PT presenting cells
XX
PS Example 1; Page 24; 39pp; English.

```
XX
CC   AAR51619 shows a region of the V3 loop (residues 315-329) of the
CC   envelope glycoprotein, gp120, of HIV-1. It represents an epitope
CC   which forms part of a hybrid-fusion polypeptide with a
CC   Fab fragment of an IgG Fab fragment.The polypeptide is capable of
CC   presenting the epitope to antigen presenting cells.
XX
SQ   Sequence   15 AA;

  Query Match             100.0%;  Score 77;  DB 15;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           ||||||||||||||||
Db       1 RIQRGPGRAFVTIGK 15


RESULT 7
AAR74603
ID   AAR74603 standard; peptide; 15 AA.
XX
AC   AAR74603;
XX
DT   01-NOV-1995  (first entry)
XX
DE   HIV-I variable loop residues 308-322.
XX
KW   MAb 5023; variable V3 loop; HIV-I; human immunodeficiency virus;
KW   cancer antigen; monoclonal antibody.
XX
OS   Human immunodeficiency virus I.
XX
PN   WO9510777-A.
XX
PD   20-APR-1995.
XX
PF   14-OCT-1994;   94WO-US11754.
XX
PR   15-OCT-1993;   93US-0138141.
XX
PA   (RAKO/) RAKOWICZ-SZULCZYNSKA E M.
PA   (RAKO/) RAKOWICZSZULCZYNSKA E M.
XX
PI   Rakowicz-szulczynska EM;
XX
DR   WPI; 1995-178531/23.
XX
PT   Detection of HIV-1 cross-reactive breast carcinoma-associated
PT   antigens - for diagnosis and anti:sense therapy of breast and
PT   gynaecological cancers
XX
PS   Disclosure; Page 48; 71pp; English.
XX
CC   MAb 5023 was developed against AA residue 308-322 of the variable
CC   loop of HIV-I (AAR74603). MAb 5023 binds to the epitope GRAF. G
CC   preceding RAF is believed to critical for internalization. MAb 5023
CC   recognised p160, p120, p42 and p24 in cancer cells. AAR74603
CC   competitively blocked binding of the MAb to the cancer antigens,
CC   indicating that at least the epitope GRAF, which is recognised by
CC   the MAb, must also be present in cancer antigens.
XX
SQ   Sequence   15 AA;

  Query Match             100.0%;  Score 77;  DB 16;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           ||||||||||||||||
Db       1 RIQRGPGRAFVTIGK 15


RESULT 8
AAR68789
ID   AAR68789 standard; peptide; 15 AA.
XX
AC   AAR68789;
XX
DT   23-AUG-1995  (first entry)
XX
DE   Cytotoxic T lymphocyte epitope 46 derived from env gp120 protein.
XX
KW   cytotoxic T lymphocyte; epitope; antigen; pathogenic; nef; gag; pol;
KW   env; gp120; gp41; HIV; cell-mediated immunity;
KW   human immunodeficiency virus; class I restricted.
XX
OS   Human immunodeficiency virus.
XX
PN   WO9428871-A.
XX
PD   22-DEC-1994.
XX
PF   07-JUN-1994;   94WO-US06394.
XX
PR   07-JUN-1993;   93US-0072718.
XX
PA   (ENDO-) ENDOCON INC.
XX
PI   Leonard RJ;
XX
DR   WPI; 1995-036067/05.
XX
PT   Implant for sustained release of pathogen-associated antigen  -
PT   forming chronic inflammatory site producing cytotoxic
PT   T-lymphocytes lysing infected cells, esp. for treating AIDS
XX
PS   Disclosure; Page 12; 35pp; English.
XX
CC   AAR68744-805 are cytotoxic T lymphocyte (CTL) class I and II  restricted
CC   epitopes derived from human immunodeficiency virus proteins. AAR68789
CC   corresponds to amino acid residues 308-322 of the env gp120 protein.
CC   These antigens are examples of peptides that can be used with an
CC   immunogenic implant. The implant is associated with an antigen
CC   associated with a pathogen and used to form a discrete, localised
CC   chronic inflammation site which acts as a local 'factory' for prodn. of
CC   CTL's which lyse cells infected with a specific pathogen. The expanded
CC   set of pathogen-specific CTL's can eradicate or prevent development of
CC   infection, and can also be used to treat or arrest the development of
CC   cancers associated with infection.
XX
SQ   Sequence   15 AA;

  Query Match             100.0%;  Score 77;  DB 16;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RIQRGPGRAFVTIGK 15
           ||||||||||||||||
Db       1 RIQRGPGRAFVTIGK 15


RESULT 9
AAR66414
ID   AAR66414 standard; peptide; 15 AA.
XX
AC   AAR66414;
XX
DT   03-AUG-1995  (first entry)
XX
DE   HIV-1 IIIB peptide 18.
XX
KW   T cell helper site; cytotoxic T cell response; neutralising antibody;
KW   human immunodeficiency virus type 1; envelope glycoprotein gp120;
KW   cluster peptide; principal neutralising determinant; IIIB isolate.
XX
```

OS Synthetic.
XX
PN WO9426785-A.
XX
PD 24-NOV-1994.
XX
PF 13-MAY-1994; 94WO-US05142.
XX
PR 14-MAY-1993; 93US-0060988.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH) US SEC DEPT HEALTH.
XX
PI Ahlers JD, Berzofsky JA, Nara P, Pendleton CD, Shirai M;
XX
DR WPI; 1995-006707/01.
XX
PT Polypeptide inducing helper T cell, cytotoxic T cell and
PT antibodies responses - to target antigen in hosts of different
PT MHC haplotypes, esp. for therapeutic or prophylactic vaccines
PT against HIV.
XX
PS Example 1; Page 33; 120pp; English.
XX
CC Synthetic peptides spanning multideterminant regions from the HIV
CC envelope protein gp160 have been designed and are designated cluster
CC peptides (PCLUS). These peptides each consist of a cluster of
CC overlapping determinants and are known to induce in vitro T cell
CC proliferation and cytokine production in mice and humans of multiple
CC MHC types. The cluster peptides were co-linearly synthesised at the
CC N-terminus of an immunodominant CTL determinant, Peptide 18 (AAR66414),
CC corresp. to part of the gp160 V3 loop and principal neutralising
CC determinant region of HIV-1 IIIB isolate.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
||||||||||||||||
Db 1 RIQRGPGRAFVTIGK 15

RESULT 10
AAW07931
ID AAW07931 standard; peptide; 15 AA.
XX
AC AAW07931;
XX
DT 31-JAN-1997 (first entry)
XX
DE gp120 peptide p18p.
XX
KW HIV; gp120; HIV-IIIB strain; HIV-1 transmission; foetal transmission;
KW neutralising antibody; passive immunisation; anti-idiotypic antibody;
KW gp41; vaccine; active immunotherapy.
XX
OS Human immunodeficiency virus type 1.
XX
PN US5556744-A.
XX
PD 17-SEP-1996.
XX
PF 24-MAR-1994; 94US-0218025.
XX
PR 24-MAR-1994; 94US-0218025.
PR 29-MAY-1992; 92US-0891451.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
PI Ugen KE, Weiner DB, Williams WV;
XX
DR WPI; 1996-432980/43.
XX
PT Determining the likelihood of maternal transmission of HIV-1 to
PT foetus - by measuring maternal reactivity with specific gp120 and
PT gp41 derived peptide(s), also used for diagnosing HIV in infants
XX
PS Example 2; Column 18; 63pp; English.
XX
CC This sequence represents a HIV gp120 peptide that can be used in the
CC method of the invention. The method of the invention is for determining
CC whether or not a mother will transmit HIV-1 to a foetus. The method
CC comprises incubating a sample from the HIV-infected mother, with a
CC collection of HIV peptides. The HIV peptides includes at least one of
CC the gp120 sequences (such as AAW07909-W07917), and at least one HIV gp41
CC derived peptide (see AAW07918-W07928). The number of peptides that
CC react with the sample is determined, and this number is compared with a
CC standard that shows pattern reactivity for a patient of transmission
CC status. A non-transmissive HIV sample is indicated if the test sample
CC reacts with twice as many peptides as the standard. The method detects
CC the presence of neutralising antibodies that protect against mother to
CC infant transmission of HIV. These sequences can also be used in
CC vaccines to protect against transmission. Antibodies against these
CC sequences can be used for passive immunisation, and to generate
CC anti-idiotypic antibodies for use in vaccines or active immunotherapy.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
||||||||||||||||
Db 1 RIQRGPGRAFVTIGK 15

RESULT 11
AAW05535
ID AAW05535 standard; Peptide; 15 AA.
XX
AC AAW05535;
XX
DT 17-JAN-1997 (first entry)
XX
DE HIV-1 gp120 peptide (aa308-322).
XX
KW gC1q receptor; gC1q-R; HIV-1; gp120; immunogen; vaccine.
XX
OS Human immunodeficiency virus type 1 strain HXB2R.
XX
PN WO9630400-A1.
XX
PD 03-OCT-1996.
XX
PF 22-MAR-1996; 96WO-US03905.
XX
PR 24-MAR-1995; 95US-0410360.
XX
PA (TANO-) TANOX BIOSYSTEMS INC.
XX
PI Fung MSC, Kim YW, Sun BNV, Sun CRY, Yu L;
XX
DR WPI; 1996-455274/45.
XX
PT New gC1q receptor-based, HIV-1 gp 120 binding peptide(s) - for
PT preventing and treating HIV-1 infection
XX
PS Claim 10; Page 49; 53pp; English.
XX
CC A peptide (AAW05535) corresponds to amino acids 308-322 of the V3
CC region of gp120 from HIV-1 strain HXB2R2. It was used to examine

```
CC   the binding of gC1q receptor (gC1q-R) (see also AAW05534) to HIV-1
CC   gp120.  Anti-HIV-1 gp120 V3 domain murine monoclonal antibody
CC   BAT123 was able to react with gp120 bound to gC1q-R, showing that
CC   the binding of gC1q-R to gp120 does not involve the V3 region of
CC   gp120; the binding site was localised to amino acids 444-459 (see
CC   also AAW05533) of gp120.
XX
SQ   Sequence   15 AA;

  Query Match             100.0%;  Score 77;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db      1 RIQRGPGRAFVTIGK 15


RESULT 12
AAR92007
ID   AAR92007 standard; Protein; 15 AA.
XX
AC   AAR92007;
XX
DT   27-SEP-1996  (first entry)
XX
DE   HIV-1 V3 loop epitope, for insertion in Mycobacterium alpha antigen.
XX
KW   Mycobacterium bovis BCG; AIDS vaccine; surface protein;
KW   alpha antigen; Human immunodeficiency virus type 1; fusion protein;
KW   gp120 epitope; V3 loop.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO9604009-A1.
XX
PD   15-FEB-1996.
XX
PF   31-JUL-1995;   95WO-JP01515.
XX
PR   29-JUL-1994;   94JP-0178462.
XX
PA   (AJIN ) AJINOMOTO CO INC.
PA   (NINA-) JAPAN AGENCY NAT INST HEALTH.
XX
PI   Chujo Y,  Honda M,  Matsuo K,  Tasaka H,  Yamazaki A;
PI   Yamazaki S;
XX
DR   WPI; 1996-129127/13.
DR   N-PSDB; AAT16048, AAT16049.
XX
PT   BCG containing vaccine secretes chimeric protein containing foreign
PT   antigen  - has enhanced immunogenicity and antigenicity esp. when
PT   used as an anti-AIDS vaccine
XX
PS   Example 2; Page 17; 56pp; Japanese.
XX
CC   Antigenic peptides can be inserted into the alpha-antigen sequence
CC   of a Mycobacterium and secreted from an appropriately transformed
CC   M.bovis BCG cell. The resulting chimeric antigen has greatly
CC   enhanced antigenicity and immunogenicity and is recognised in vivo
CC   by B-cells which recognise the alpha-antigen. The present sequence
CC   is that of a HIV-1 gp120 V3 loop epitope which was incorporated
CC   into the alpha antigen. M.bovis BCG cells secreting a
CC   chimeric protein comprising the epitope sequence are useful as
CC   anti-AIDS vaccines.
XX
SQ   Sequence   15 AA;

  Query Match             100.0%;  Score 77;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db      1 RIQRGPGRAFVTIGK 15


RESULT 13
AAR92033
ID   AAR92033 standard; peptide; 15 AA.
XX
AC   AAR92033;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Hydrophilic peptide for epimorphin modification (5).
XX
KW   Epimorphin; human; mouse; wound; burn; epithelial tissue;
KW   diagnosis; treatment; morphogenetic abnormality; cosmetic;
KW   hair growth stimulator.
XX
OS   Synthetic.
XX
PN   EP698666-A2.
XX
PD   28-FEB-1996.
XX
PF   20-JUN-1995;   95EP-0304270.
XX
PR   31-MAR-1995;   95JP-0099980.
PR   21-JUN-1994;   94JP-0162874.
PR   31-MAR-1995;   95JP-0099979.
XX
PA   (SUME ) SUMITOMO ELECTRIC IND CO.
XX
PI   Hirai Y,  Koshida S,  Oka Y;
XX
DR   WPI; 1996-118213/13.
XX
PT   Novel polypeptide containing an epimorphin functional domain  - has
PT   possible benefits in epithelial tissue treatments, e.g. burns and
PT   for artificial organs
XX
PS   Claim 8; Page 57; 62pp; English.
XX
CC   New polypeptides contain a first portion of 5-99 amino acids joined
CC   to a second portion contg. at least a functional domain of
CC   epimorphin.  The first portion may be selected from the peptides
CC   given in AAR92029 to AAR92036.  The second portion may be full-length
CC   epimorphin (see AAR92037 to AAR92042 for human and mouse epimorphins).
CC   Fragments of epimorphins given in AAT16083 to AAT16090 are used in the
CC   prodn. of modified epimorphins.
CC   The modified epimorphins are useful for the development of diagnosis
CC   and treatment of morphogenetic abnormalities of epithelial tissue or
CC   novel remedies for wounds, eg burns, after surgery and for artificial
CC   organs.  They may also be used as components of cosmetics, hair
CC   growth stimulators, etc.
XX
SQ   Sequence   15 AA;

  Query Match             100.0%;  Score 77;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RIQRGPGRAFVTIGK 15
          |||||||||||||||
Db      1 RIQRGPGRAFVTIGK 15


RESULT 14
AAW24219
ID   AAW24219 standard; peptide; 15 AA.
XX
AC   AAW24219;
XX
```

DT 17-MAR-1998 (first entry)
XX
DE CD4+ T-lymphocyte epitope to HIV-1 V3 loop derived peptide V3-LAI-P18.
XX
KW T-lymphocyte epitope; diagnosis; antigen; infectious disease;
KW delayed-type hypersensitivity assay; vaccine development.
XX
OS Synthetic.
OS Human immunodeficiency virus.
XX
PN WO9727462-A2.
XX
PD 31-JUL-1997.
XX
PF 27-JAN-1997; 97WO-US01084.
XX
PR 26-JAN-1996; 96US-0010679.
XX
PA (USSA) US DEPT ARMY GOVERNMENT US ARMY MEDICAL.
XX
PI Brix DL, Sitz KV;
XX
DR WPI; 1997-393814/36.
XX
PT Peptide fragments containing antigen epitope(s) used to trace
PT diseases - used in a delayed-type hypersensitivity assay, for in
PT vivo mapping of human T-lymphocyte epitope(s) e.g. for diagnosis,
PT vaccine development etc
XX
PS Disclosure; Page 6; 14pp; English.
XX
CC Peptide fragments AAW24217-20 were used to demonstrate a new method
CC of tracing sources of infectious diseases. The method comprises
CC preparing a short (9-50 amino acid) peptide containing at least one
CC non-conserved epitope of an organism, injecting a composition containing
CC the peptide intradermally into a test subject in a delayed-type
CC hypersensitivity (DTH) assay and observing the injection site at
CC intervals for induration. In this example CD4+ T-lymphocyte
CC epitopes to the HIV-1 V3 loop were mapped by existing in vitro technique
CC for two existing HIV infected individuals and used to design peptides
CC AAW24217-20. The method allows the T-lymphocyte epitopes of a large
CC antigen to be determined in vivo in humans. The method is useful in
CC medicine e.g. in diagnosis, monitoring and treatment design for
CC infectious disease exposure, active autoimmune disease, allergic diseases
CC and malignancy. It is especially useful for tracing infectious diseases
CC e.g HIV, particularly when a sequence is present only in certain strains
CC of an organism, and developing suitable vaccines. Vaccinated individuals
CC can also be tested to verify protection against a particular strain.
CC The method allows in vivo mapping of T-lymphocyte epitopes, not
CC previously possible. The method is simpler, more rapid and more
CC sensitive. It can also be applied in a variety of environments e.g.
CC undeveloped regions since specialist equipment is not required.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
||||||||||||||||
Db 1 RIQRGPGRAFVTIGK 15

RESULT 15
AAW22031
ID AAW22031 standard; peptide; 15 AA.
XX
AC AAW22031;
XX
DT 20-FEB-1998 (first entry)
XX
DE Antigenic human immunodeficiency virus peptide P18.
XX
KW Antigenic peptide; human papillomavirus; MAGE gene; BAGE-1 peptide; P18;
KW human immunodeficiency virus; cancer antigen; tyrosinase; signal protein;
KW anthrax lethal factor; LF; toxin; cationic fusion peptide; translocation;
KW gene therapy; polycationic affinity handle; therapeutic protein; LFN.
XX
OS Human immunodeficiency virus.
XX
PN WO9723236-A1.
XX
PD 03-JUL-1997.
XX
PF 13-DEC-1996; 96WO-US20463.
XX
PR 07-JUN-1996; 96US-0019275.
PR 13-DEC-1995; 95US-0008518.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Ballard JD, Blanke SR, Collier RJ, Lyszak EL, Milne JC;
PI Starnbach MN;
XX
DR WPI; 1997-350782/32.
XX
PT Introducing therapeutic proteins, especially antigens, into cells -
PT using toxin molecules and/or polycationic handles for delivery
XX
PS Claim 15; Page 36; 67pp; English.
XX
CC This is the antigenic human immunodeficiency virus peptide P18. This
CC antigenic compound can be introduced into the cytoplasm of a cell by a
CC new method where the cell is contacted with a fusion molecule comprising
CC a delivery molecule. The delivery molecule can either be a polycationic
CC affinity handle, LFN (the protective antigen binding domain of anthrax
CC lethal factor) or a toxin delivery molecule related to LFN. The antigenic
CC compound is linked to either of the delivery molecules by a covalent
CC bond. The B moiety of a toxin enhances delivery of the antigenic compound
CC into a cell. The anthrax toxin system of the invention eliminates the
CC need to generate fusion proteins with a toxin B moiety, which alleviates
CC problems associated with incorrect folding of lengthy fusion proteins.
CC Small cationic fusion peptides substituted for LFN may reduce the
CC possibility of steric interference with the biological activity of the
CC translocated protein. The method is used for the introduction of
CC antigens, e.g. MHC class I antigens or any other therapeutic protein,
CC e.g. toxin molecules, apoptosis-inducing molecules or signalling
CC proteins into the cells.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQRGPGRAFVTIGK 15
||||||||||||||||
Db 1 RIQRGPGRAFVTIGK 15

Search completed: March 10, 2003, 17:51:12
Job time : 37 secs